

SEQUENCE LISTING

<110> Zyskind, Judith.
Forsyth, R. Allyn

<120> GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
ESCHERICHIA COLI

<130> ELITRA.001C1

<140> Unknown

<141> 2004-02-03

<150> 09/492,709

<151> 2000-01-27

<150> 60/117,405

<151> 1999-01-27

<160> 485

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 159

<212> DNA

<213> E. Coli

<400> 1

cagggtggtat	ggaacccaa	aatggagacg	ggaagctgaa	ccagatagtt	actggaggtg	60
atcaccagca	gatgaaataa	cgataaccag	aacaacgcct	tatagcggtg	agtttgcgag	120
aaaacgttca	tattgtacct	ttttgattaa	ccattgggg			159

<210> 2

<211> 696

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(696)

<223> n = A,T,C or G

<400> 2

gattacatca	agcgcgcggt	gggtttaccg	ggcgataaaag	tcacttacga	tccggtctca	60
aaagagctga	cgattcaacc	gggatgcagt	tccggccagg	cggttgaaaa	cgcgctgccg	120
gtcacctact	caaacgtgga	accgagcgat	ttcgttcaga	ccttctcacg	ccgtaaatggt	180
ggggaagcga	ccagcggatt	ctttgaagtg	ccgaaaaacg	aaaccaaaga	aaatggaatt	240
cgtctttccg	agcgtaaaga	gacactgggt	gatgtgacgc	accgcattct	gacagtgccg	300
attgcgcagg	atcaggtggg	gatgtattac	cagcagccag	ggcaacaact	ggcaacctgg	360
attgttcctc	cgggacaata	cttcatgatg	ggcgacaacc	gcgacaacag	cgcggaacagc	420
cgttactggg	gctttgtgcc	ngaagcgaat	ctggtcggtc	nggcaacggc	tatctggatg	480
aacttcgata	accaagaagg	cgaatggccg	aatggctctgc	cctaantcgc	attggcgnnt	540
ccnttaatan	ccacttcctt	cnctttgtcc	ccttatggca	acacttaatt	tattntaaan	600
taatnccccg	tggetnacaa	atccccgcct	tttnttaaaa	atttcccnna	anttaaggtt	660
ggcctccagt	tgcccgnccc	aaacactttg	gncccc			696

<210> 3
 <211> 681
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(681)
 <223> n = A,T,C or G

<400> 3

ctgcagggta	atgtcgccat	taaactggcg	caggcagcca	aagagttgct	ccgcttctac	60
ccagtcggca	gcgacaactt	gcgttaaagt	cgcaaaatta	tcattctgcac	tcactgcgtg	120
acgtaagcgg	atggagtggc	cggaacctc	atagtgaccg	cccaccagtt	ggcctgcatc	180
gctttgtagc	gtacgcgcgg	cattggcaat	aagattcaga	tactcagact	cttccggggc	240
cttcgccagc	ataaaagagg	aggatgctcg	cgatatgcagc	aactgctcca	gcgcaaattg	300
cagccgcggg	tgagtatcac	tgaataaagg	atcgttttcg	tcaatcaa	gtggctgagc	360
aaatatttcc	tgatagctat	cggtatcagg	aaccagggtca	cgccatgcaa	gtttcgtaat	420
ggtcaaagtt	gatgtttttt	agtctgttgt	caaagccgcn	attataccng	taaccggcac	480
tacagcacac	gtagaaagca	cccgacaata	ctcctggcat	gggcgttaaa	gctcacagga	540
tggagatctt	ttcttcaactg	gcctaaaaag	ctgatattct	gtaaagagtt	acacngtaac	600
attgagatcg	ctatgaaata	tcaacaactt	ggaaaatctt	gnaaagcngg	ttggaaaatg	660
gaaagtatct	ggttaagaag	c				681

<210> 4
 <211> 289
 <212> DNA
 <213> E. Coli

<400> 4

ggcagaattt	tacgtgacc	aatgacgcga	cgacgtggca	tggaaatact	ccgttggttaa	60
ttcaggattg	tccaaaactc	tacgagttta	gtttgacatt	taagttaaaa	cgtttggcct	120
tacttaacgg	agaaccatta	agccttagga	cgcttcacgc	catacttgga	acgagcctgc	180
ttacggctct	taacgccgga	gcagtcaagc	gcaccacgta	cggtgtggta	acgaacaccc	240
gggaggtctt	taacacgacc	gtcacggatc	aggatcacgg	agtgtctcct		289

<210> 5
 <211> 815
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(815)
 <223> n = A,T,C or G

<400> 5

gggagcttac	atcagtaagt	gaccgggatg	agcgagcgaa	gataacgcat	ctgcggcgcg	60
aaatatgaag	ggggagagcc	cttatagacc	aggtagtaca	cgtttggtta	gggggcctgc	120
atatggcccc	ctttttcaact	tttatatctg	tgcggtttta	tgccgggcag	atcacatctc	180
cgaggatttt	agaatggctg	aaattaccgc	atccctggta	aaagagctgc	gtgagcgtag	240
tggcgagggc	atgatggatt	gcaaaaaagc	actgactgaa	gctaacggcg	acatcgagct	300
ggcaatcgaa	aacatgcgta	agtcgggtgc	tattaaagca	gcgaaaaaag	caggcaacgt	360
tgctgctgac	ggcgtgatca	aaacaaaaat	cgacggcaac	tacggcatca	ttctggaagt	420
taactgccag	actgacttcg	ttgcaaaaaga	cgctgggttc	caggcggttcg	cagacaaagt	480
tctggacgca	gctgttgctg	gcaaaatcac	tgacgttgaa	gttctgaaag	cacagttcga	540
agaagaacgt	gttgcgctgg	tagcgaaaat	tggtgaaaac	atcaacattc	gccgcgttgc	600

tgcgctggaa	ggcgacgttc	tgggttctta	tcagcacggt	gcgcgatatcg	gccgttctgg	660
ttgctgctaa	aagcgctgac	gaagaactgg	ttaaacacat	cgttttgacc	tttgttgcaa	720
gccaagccag	aattcagaga	aactttccgc	ttcaccggag	gtcccaccca	cangganccc	780
cgattttntc	agcatggtgg	tcttctnccg	gagtt			815

<210> 6
 <211> 403
 <212> DNA
 <213> E. Coli

<400> 6						
caacactatt	ttgttgaccg	gaaaatggaa	cactttccgc	aatgcctggt	gctatcacgc	60
ttaaaccatt	tcattgcat	ttacacagaa	cggacgtcct	gtcgagtat	attaagtcgt	120
cgatagaaac	aagcattgaa	aggcacagca	gtagtcaaac	agtgtgaaac	gctactggcg	180
ccttacagcg	caaaaaggct	ggtgactaaa	aagtcaccag	ccatcagcct	gattttctcag	240
gctgcaaccg	gaagggttgg	cttattttaac	ttcaacttca	gcgccagctt	cttcagagc	300
ttttttcagt	gcttctgcgt	cgtctttgct	cacgccttct	ttcagagcag	ccggtgcaga	360
ttctaccagg	tctttagctt	ctttcagacc	caggccagtt	gcg		403

<210> 7
 <211> 149
 <212> DNA
 <213> E. Coli

<400> 7						
gagctttttt	cagtgccttct	gcgtcgtctt	tgctcacgcc	ttctttcaga	gcagccggtg	60
cagattctac	cagggtcttta	gcttctttca	gaccagggcc	agttgcgcca	cgtagctgctt	120
tgataacagc	aactttgtta	gcgccagca				149

<210> 8
 <211> 742
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(742)
 <223> n = A,T,C or G

<400> 8						
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actttccgca	atgcctgttg	ctatcacgct	taaaccatth	cattgagatt	tacacagaac	120
ggacgtcctg	tcgcagtata	ttaaagtcgtc	gatagaaaca	agcattgaaa	ggcacagcag	180
tagtcaaaca	gtgtgaaacg	ctactggcgc	cttacagcgc	aaaaaggctg	gtgactaaaa	240
agtcaccagc	catcagcctg	attttctcagg	ctgcaaccgg	aagggttggc	ttattttaact	300
tcaacttcag	cgccagcttc	ttccagagct	tttttcagtg	cttctgcgtc	gtctttgctc	360
acgccttctt	tcagagcagc	cggtgcagat	tctaccaggt	ctttagcttc	tttcagaccc	420
aggccagttg	cgccacgtac	tgctttgata	acagcaactt	tgttagcgcc	agcagctttc	480
agaattacgt	cgaattcagt	tnntttcttca	gcagcttcaa	ccggggccagc	agctacagct	540
acagcagcag	caagcggaac	caccgaatth	ttcttccatt	gcagagatca	gttctacaac	600
cgtccattac	agacatagct	gcaactgctt	caatgattth	gatcttttagt	ggatagacat	660
ttaaattgtt	cctgaattat	caagaaataa	gtnttatagc	taagccgaaa	tgcgttaaaa	720
aagataactg	ngattaaagc	ag				742

<210> 9
 <211> 421
 <212> DNA

<213> E. Coli

<400> 9

agtagtcaaa	cagtgtgaaa	cgctactggo	gccttacagc	gcaaaaaggc	tggtgactaa	60
aaagtcacca	gccatcagcc	tgattttctca	ggctgcaacc	ggaaggggtg	gcttatttaa	120
cttcaacttc	agcgccagct	tcttccagag	cttttttcag	tgcttctgcg	tcgtctttgc	180
tcacgccttc	tttcagagca	gccgggtgcag	attctaccag	gtcttttagct	tctttcagac	240
ccaggccagt	tgcgccacgt	actgctttga	taacagcaac	tttgtttagcg	ccagcagctt	300
tcagaattac	gtcgaattca	gttttttctt	cagcagcttc	aaccggggcca	gcagctacag	360
ctacagcagc	agcagcggaa	acaccgaatt	tttcttccat	tgcaagagatc	agttctacaa	420
c						421

<210> 10

<211> 126

<212> DNA

<213> E. Coli

<400> 10

agagcttttt	tcagtgtctt	tgcgtcgtct	ttgctcacgc	cttctttcag	agcagccggg	60
gcagattcta	ccagggtctt	agcttctttc	agaccagggc	cagttgcgcc	acgtactgct	120
ttgata						126

<210> 11

<211> 262

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(262)

<223> n = A,T,C or G

<400> 11

ctgcaaccgg	aagggttggc	ttatttaact	tcaacttcag	cgccagcttc	ttccagagct	60
tttttcagt	cttctgcgtc	gtctttgctc	acgccttctt	tcagagcagc	cgntgcagat	120
tctaccaggt	cttttagcttc	tttcagaccc	aggccagttg	cgccacgtac	tgctttgata	180
acagcaactt	tgtttagcgcc	agcagctttc	agaattacgt	cgaattcagt	tttttcttca	240
gcagcttcaa	ccgggccagc	ag				262

<210> 12

<211> 202

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(202)

<223> n = A,T,C or G

<400> 12

gcgcataccc	tgcaagcatc	gcccgatgga	gatcagggtc	gcagaacgct	gtaccgcttt	60
gtagggtggt	ttaccgggtg	tcagatccgg	gaagatgaac	acggtagcgc	gacctgcaac	120
cggagagttc	ggcgcttttg	attncgcaac	gtcagccatt	accgcagcgt	cgtactgcag	180
cggaccggcg	atcatcaggt	ca				202

<210> 13

<211> 261

<212> DNA
 <213> E. Coli

<400> 13
 tctaggagta agaatagctt caaattcagc agttgacagt ggcataaacg taactggtga 60
 cttttgcccg gcatgacgcc gggctttttt tattattccg tgacttccag cgtagtgaag 120
 gcaaacttct cgccatcaaa tagccctga ctggttagtt ttagcgcggg gatcactggc 180
 agagaaagaa acgccatctg aataaacggc tcatcgggta acggaccgca ttcacgggcg 240
 gcggctttca aggcgtcaat t 261

<210> 14
 <211> 224
 <212> DNA
 <213> E. Coli

<400> 14
 ttcttttttt cgtcaacggt gtccagaatc attttattta cctcggggta cttatgctga 60
 tttttattat tatggggaag gtgttattta tgagtttcat ttatgccgta acgacaatga 120
 actcggaat tagtataagc agcgcgagaa taataatcat tgtgcaaag ctaattta 180
 taatactatt taaatattat tttagagcata tgcacataag gttg 224

<210> 15
 <211> 232
 <212> DNA
 <213> E. Coli

<400> 15
 aattcccttc tttttttcgt caacggtgtc cagaatcatt ttatttacct cgggtactta 60
 tgctgatttt tattattatg gggaagggtg tatttatgag tttcatttat gccgtaacga 120
 caatgaactc gggaattagt ataagcagcg cgagaataat aatcattgtg caaatgctaa 180
 ttttaattaat actatttaaa tattattttg agcatatgca cataagggtg gg 232

<210> 16
 <211> 212
 <212> DNA
 <213> E. Coli

<400> 16
 aatagcgggt atgcacgcct ttcttttttt cgtcaacggt gtccagaatc attttattta 60
 cctcggttac ttatgctgat ttttattatt atggggaagg tgttatttat gaggttcatt 120
 tatgccgtaa cgacaatgaa ctcggaatt agtataagca gcgcgagaat aataatcatt 180
 gtgcaaatgc taatttaatt aatactattt aa 212

<210> 17
 <211> 433
 <212> DNA
 <213> E. Coli

<400> 17
 ccttgtaaat tatcgcccggt ggcataaaaa ctgctgcca acgccgtctt tgccagcagc 60
 caggccataa atgccaccag aattatcgct aaccaacca ttgctgaaac gccaagcagc 120
 agcggggcgg agagctggtt cagttcggcg ggtaaccctt caatccattt gccgccagtc 180
 cacagcaaca tgatgcctct gtacaaccct aacgtgccaa ggggtggcaac aatggcaggg 240
 atcttttagcc acgcgaccag gacaccgttg aaaaatcccg cgagcaaacc aagcagtaaa 300
 gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
 gcgcacattc cggtaatcga acccaactgaa acatcaatat tgcgcgtaag cattaccagc 420
 gtcgcgccca ttg 433

<210> 18
 <211> 658
 <212> DNA
 <213> E. Coli

<400> 18
 cgtgcgcttc cggttgtggc aaccgcgcaa atggcgcggc ggtaagtatg gcgggggttat 60
 tccttccccg ttgaggacac cgggttgtca ggttgaccat acgcttaagt gacaacccccg 120
 ctgcaacgcc ctctgttatc aattttctgg tgacgtttgg cggtatcagt tttactccgt 180
 gactgctctg ccgccctttt taaagtgaat tttgtgatgt ggtgaatgcg gctgagcgca 240
 cgcggaacag ttaaaaccaa aaacagtgtt atgggtggat tctctgtatc cggcgttaat 300
 tgttaactgg ttaacgtcac ctggaggcac caggcactgc atcacaaaat tcattgttga 360
 ggacgcgata atgaaaacgt tattaccaaa cgtaatacgc tctgaagggt gttttgaaat 420
 tgggtgtcact atcagtaacc cagtattttac tgaagatgcc attaacaaga gaaaacaaga 480
 acgggagcta ttaataaaaa tatgcattgt ttcaatgctg gctcgtttac gtctgatgcc 540
 aaaaggatgt gcacaatgaa ttcagcattt gtgcttgttc tgacagtttt tcttgtttcc 600
 ggagagccag ttgatattgc agtcaagtgg tcacaggaca atgcaggagt gtatgact 658

<210> 19
 <211> 588
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(588)
 <223> n = A,T,C or G

<400> 19
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 cacgcggaac agttaaacc aaaaacagtg ttatgggtgg attctctgta tccggcgtta 120
 attgttaact ggtaacgtc acctggaggc accaggcact gcatcacaaa attcattgtt 180
 gaggacgca taatgaaaac gttattacca aacgttaata cgtctgaagg ttgttttgaa 240
 attggtgtca ctatcagtaa cccagtattt actgaagatg ccattaacaa gagaaaacaa 300
 gaacgggagc tattaaataa aatatgcatt gtttcaatgc tggctcgttt acgtctgatg 360
 ccaaaaggat gtgcacaatg aattcagcat ttgtgcttgt tctgacagtt tttcttgttt 420
 ccggagagcc agttgatatt gcagtcagtg ttcacaggac aatgcangag tgtatgactg 480
 cagcaacccc aacagaaaaat tcccggtaac tgttaccggc tcgataaagt tattcaccag 540
 gataatatcg aaatcccggc aggtctttaa aacagttccg taataaat 588

<210> 20
 <211> 101
 <212> DNA
 <213> E. Coli

<400> 20
 gatccagcaa gaagatgcgg ttgtaccgtc atcacgcaga tgcgcaaagc tactcagcaa 60
 ctgacctttc ttcgcaataa gcacgccatt agcgtcatag a 101

<210> 21
 <211> 465
 <212> DNA
 <213> E. Coli

<400> 21
 tcgcgtgttt accttcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct 60

gcggtttacc	tacgttcgct	tcaacgttga	attcacgctt	catacgggtca	acgatgatgt	120
cgaggtgcag	ttcgcccata	cccgcgatga	tggctctggt	agattcttcg	tcagtccata	180
cacggaaaga	cgggtcttct	ttagccagac	ggcccagagc	cagacccatt	ttttcctggt	240
cagctttggt	tttcggttca	actgcgatgg	agattaccgg	ctcagggaat	tccatacgtt	300
ccagaatgat	cggcgcaccc	gggtcacaca	gggtgtcacc	agtgggttacg	tcttttcagac	360
cgatagcagc	agcgatgtcg	cccgcgcgaa	cttctttgat	ctcttcacgt	ttgttagcgt	420
gcatctgaac	gatacgaccg	aaacgctcac	gtgcagcttt	cacgg		465

<210> 22
 <211> 859
 <212> DNA
 <213> E. Coli

 <220>
 <221> misc_feature
 <222> (1)...(859)
 <223> n = A,T,C or G

<400> 22						
tgatcggtc	aagcagaact	ggtttcgctt	tcttaaagcc	ttctttaaaag	gcgatagaag	60
cagccagttt	aaacgccagt	tcagaggagt	caacgtcatg	gtaagaaccg	aagtgcagac	120
gaatacccat	gtctactacc	gggtagcctg	ccagcggacc	tgctttcagc	tgttcctgga	180
tacctttatc	aacggccggg	atgtattcgc	cagggattac	accaccttta	atgtcgttga	240
tgaactcgta	gcctttcggg	tttgaacccg	gctccagcgg	gtacatgtcg	ataacaacat	300
gaccatactg	accacgacca	ccagactggt	tcgcgtgttt	accttcaaca	tcggtaactt	360
tctggcggat	agtttcacgg	taagcaacct	gcggtttacc	tacgttcgct	tcaacgttga	420
attcacgctt	catacgggtca	acgatgatgt	cgaggtgcag	ttcgcccata	cccgcgatga	480
tggctctggt	agattcttcg	tcagtccata	cacggaaaaga	cgggtcttct	ttagccagac	540
gggccanagc	cagacccatt	ttttcctggt	cagctttggt	tttcggtcaa	ctgcgatgga	600
gattaccggc	tcanggaatt	tccatacctt	ccaggaatga	tcggcgcatt	ccggtcaaac	660
angnggtacc	aggggggtac	ntnttttttaa	nancgattgc	cagcancgga	tntnncccgn	720
gccnaacttc	tttggaacnn	tttaccggtt	ggtaaccngc	ctttttnaacn	atccaaccga	780
aaaagngtta	anngccantt	ttccnggngt	tnanntncgg	nttcccngaa	ntaaccncnc	840
cggggttnaac	ccngnaaaa					859

<210> 23
 <211> 269
 <212> DNA
 <213> E. Coli

<400> 23						
ctttcttaaa	gccttcttta	aaggcgatag	aagcagccag	tttaaacgcc	agttcagagg	60
agtcaacgtc	atggtaagaa	ccgaagtgca	gacgaatacc	catgtctact	accgggtagc	120
ctgccagcgg	acctgctttc	agctgttcct	ggataccttt	atcaacggcc	gggatgtatt	180
cgccagggat	tacaccacct	ttaatgtcgt	tgatgaactc	gtagcctttc	gggtttgaac	240
ccggctccag	cgggtacatg	tcgataaca				269

<210> 24
 <211> 330
 <212> DNA
 <213> E. Coli

<400> 24						
gttttgggga	gatgtaaggg	ctaactctgaa	tggctgcatt	ccttgtttaa	ggaaaaacga	60
atgactgatt	gccgatacct	gattaaacgg	gtcatcaaaa	tcatcattgc	tgttttacag	120
ctgatccttc	tgttcttata	acacaaggaa	acgtacttaa	ggtgcgtccg	gtgaaccagt	180
cggacgcacc	tttaataact	ataaataagt	gtctgggcag	atactatata	aattaactta	240

gtgaatgatt atgctaattgt catcaattaa ataaatataa tggcggttaag gcttcccagt	300
aatataatta atactctact tccagagtag	330

<210> 25
 <211> 471
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(471)
 <223> n = A,T,C or G

<400> 25	
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atgactgatt gccgatacct gattaaacgg gtcacaaaa tcatcattgc tgttttacag	120
ctgatccttc tgttcttata acacaaggaa acgtacttaa ggtgccgtcc ggtgaaccag	180
tcggacgcac ctttaataac tataaataag tgtctgggca gatactatat aaattaactt	240
agtgaatgat tatgctaattg tcatcaatta aataaatata atggcgtaa ggcttcccag	300
taatataatt aatactctac ttccagagta gaatattaaa ttttatccgc gtggtgcatc	360
agcacaaatt tatcccacaa ctgttcttct gtctcgacat gcccccgat ctttnacaaa	420
tantattggg ggattnggcc cncctttttg ncagggttggg gtcntctnat g	471

<210> 26
 <211> 379
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(379)
 <223> n = A,T,C or G

<400> 26	
natctgantg gctgcattcc ttgtttaagg aaaccggaat gactgattgc cgatacctga	60
ttaaaccgggt catcaaaaatc atcattgctg ttttacagct gatccttctg ttcttataac	120
acaaggaaac gtacttaagg tgcgtccggt gaaccagtcg gacgcacctt taataactat	180
aaataagtgt ctgggcagat actatataaa ttaacttagt gaatgattat gctaattgtca	240
tcaattaaat aaatataatg gcgttaaggc ttcccgagtaa tataattaat actctacttc	300
cagagtagaa tattaaattt tatccgcgtg gtgcatcagc acaaatattt cccacaactg	360
ttcttctgtc tcgacatgc	379

<210> 27
 <211> 799
 <212> DNA
 <213> E. Coli

<400> 27	
aaagatgatg tgatgagaaa gtcaatttga ataagacaat attaagagct aaaaaaatgt	60
caaaaaacac taaatcaaaa aataatggca ttagaaaata taatgcgaaa acggaggtga	120
aattagttta ttccaatga ggaaaatctc ccggcgaaaa aaccgggaga tgaaagtgtg	180
atgggtatca aataaacaac agaggagaaa tttttaacgc agccattcag gcaaactcgtt	240
taatcccatt gcctggcgga taagttgcgg cttaacgcca ggaagcgtgt cggccagttt	300
caaaccaata tcacgcagca gttttttcgc cggattggta ccggaaaaca gatcgcggaa	360
tccttgcata ccagccagca tcaacgcgc actgtgcttg cggctacgct catagcgacg	420
cagataaatg tactgcccga tgtctgggat ccgtcgacct gcagccaagc ttgggctttt	480
cagcctgata cagattaaat cagaacgcag aagcggctctg ataaaacaga atttgccctgg	540

cggcagtagc	gcggtggtcc	cacctgaccc	catgccgaac	tcagaagtga	aacgcccgtg	600
gcgcccgatg	gtagtgtggg	gtctcccat	gcgagagtag	ggaactgcc	ggcatcaaat	660
aaaacgaaag	gctcagtcga	aagactgggc	ctttcggttt	atctgggtgt	tgtcgggtgaa	720
cgctctctga	gtaggacaaa	tccgccggga	gcggattttg	aacgttgcca	aacaaccggc	780
cgggaaagg	gtgggggct					799

<210> 28
 <211> 636
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(636)
 <223> n = A,T,C or G

<400> 28						
aggggggtttg	ttgtgggcaa	tgatgcattt	aagttatcgt	ctgcagatag	aggagatatt	60
acaataaaca	acgaatcagg	gcatttgata	gtcaataccg	caattctatc	aggagatata	120
gtcactctaa	gaggaggaga	aattagggtg	gtattatagc	ttgtgcgcgc	catgattggc	180
gcgcaattta	aacttagtgc	tttacatcgc	tattgtcttg	atttctttga	attattttat	240
aaattaaaaa	aacgactgtt	atgtataagc	aaaggctcgaa	cgaaaaatac	attccaaata	300
aatgcttgct	taaatctcta	tatccttccc	cgaaaaatga	cacataaaat	tgagatattc	360
caaaaagaga	tactacaaat	aaagatgcct	ttatttttatt	atttctaata	aaaatagaag	420
caataaaaaa	taataacaat	gatataaatc	taatgttttt	aaatatattg	tcttttatgt	480
tagtaatagt	cgttagtatg	tttgattctc	catatattac	gtgtagtttt	ttatatacat	540
ggaaataatt	ntctttatac	tgagacatca	caccatcatc	aatggaagt	ttgaagatgg	600
tgcttggttt	gctaaccaat	aaaaagagt	cattcg			636

<210> 29
 <211> 757
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(757)
 <223> n = A,T,C or G

<400> 29						
cagcggtcgt	atttttagca	tggtttttta	ttggcggcta	tgctgccccg	ggagcataaa	60
gatgaaaaaa	acaacgatta	ttatgatggg	tgtggcgatt	attgtcgtac	tcggcactga	120
gctgggatgg	tggtaacgtc	acctctaaaa	aatagcaaag	gctgcctgtg	tcgagccttt	180
gtgcaattta	agcgtaact	tttaatcttc	ctgtagataa	atagcacgac	aatcgcacca	240
ataacggcaa	ccacgaagct	gccaaaattg	aagccatcga	ctttaccaa	gccaaacagc	300
gtgctgatcc	atccgccgac	tacggcaccg	actatcccca	gcaggatagt	cataaagaat	360
ccacctccat	ctttacctgg	catgatccac	ttcgccagaa	taccggcaat	aagccaaaaa	420
ataatccatg	acagaatgcc	cattgtttcc	tcacttatct	gttttgcat	agcgggttag	480
tcgctgataa	aaagcatagc	acaacatcgg	gagggcaaga	tttgtgacga	gcatcacgga	540
ggtttttttt	gcgatggcgc	agaaattgcg	ccatcaacga	tcagtataa	ttaccaacca	600
caaacatcat	gttcgttttc	cgtgtcataa	gaaccgtacg	ggattcacca	gatcttttat	660
cacttcaagc	cggcacttct	ggcaccagca	aagtcacgcg	cgtctctggt	tcataatcga	720
ccggaaacgc	cattgctggt	attggtgaac	gtcacgg			757

<210> 30
 <211> 392
 <212> DNA

<213> E. Coli

<400> 30

aattacagaa	aaaggaggca	ataticgggta	aaggcattag	cccgacgaat	acgtcgggct	60
acaaatatta	ttgtgctgca	ggtgtttttag	cgggttggtg	atccacaggt	tctaactgga	120
agaccacatc	gacctgatca	tcaaactgaa	tagcggcctg	ctcgtaagtt	tcctgggcgg	180
acaccggcgc	ggcatcggct	ttcatcatcc	gcaccattgg	gctgggctga	tagttggaaa	240
catggtagcg	cacgctatat	accggcccca	gtttacgatg	aaagccgttc	gccagttcct	300
gcgcctgatg	aatcgcgtta	tcaatcgctg	ccttacgcgc	tttgtcttta	taggcattccg	360
gctgcgccac	gcccagcgac	acagaacgaa	tt			392

<210> 31

<211> 351

<212> DNA

<213> E. Coli

<400> 31

ctatccttga	tgaaccgcg	agcaaagata	ggtgattacg	tcatggtttt	acagaaaatt	60
acagaaaaag	gaggcaatat	cgggtaaagg	cattagcccg	acgaatacgt	cgggctacaa	120
atattattgt	gctgcagggt	ttttagcggg	ttgttgatcc	acaggttcta	actggaagac	180
cacatcgacc	tgatcatcaa	actgaatagc	ggcctgctcg	taagtttcct	gggcggacac	240
cggcgcggca	tcggctttca	tcatccgcac	cattgggctg	ggctgatagt	tggaaacatg	300
gtagcgcacg	ctatataaccg	gccccagttt	acgatgaaag	ccgttcgcca	g	351

<210> 32

<211> 762

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(762)

<223> n = A,T,C or G

<400> 32

aattatgaaa	cactgtcttg	aatcgtctga	atgacgggca	catttgcgag	cacgcatcca	60
gtaataacac	aggaaactat	tttatctacg	cgttagcgat	agactgcttg	catggcgaaa	120
ggaggtaagc	cgacgatattc	agcgggacgc	tgaaccgga	aagcccctcc	cgagggaagg	180
gccataaata	aggaaagggt	catgatgaag	ctactcatca	tcgtggtgct	cttagtcata	240
agcttccccg	cttactaaga	ctaccagggc	gggggaaacc	ccgctctacc	ctcactcctg	300
aaagtatgcc	ttcacgataa	gattgtcaat	ccgcaggctt	tgtagtctgc	gatectgcc	360
gcaaataattc	tttgcgagtc	gttacgcaat	aatcacagag	gaaactat	tattcacgcg	420
ttagcgatag	actgcattca	gggcgaaagg	aggtaagccg	atgatttcag	cgggacgctg	480
aaacgggaaa	gcctctccc	gagaagagg	cttttaataa	ggaaagggtt	atgatgaagc	540
acgtcatcat	actgggtgata	ctcttagtga	ttagcttcca	ggcttactaa	gaacaccagg	600
gggaggggga	aacctcttcc	taaccctcac	ttctgaaatt	gggtgctatg	acgctggcgt	660
tactgcttan	cgctaccagt	ttgtctgccc	tggcggttgt	aacgccagat	cggtagccgt	720
ttggatat	taatgaaagc	cgacaaatca	atcancgtga	cg		762

<210> 33

<211> 293

<212> DNA

<213> E. Coli

<400> 33

gcacatttgc	gagcacgcat	ccagtaataa	cacaggaaac	tattttatct	acgcgttagc	60
gatagactgc	ttgcatggcg	aaaggaggta	agccgacgat	ttcagcggga	cgctgaaacg	120

ggaaagcccc	tcccagaggaa	ggggccataa	ataaggaaa	ggatcatgatg	aagctactca	180
tcacgcgtggt	gctcttagtc	ataagcttcc	ccgcttacta	agactaccag	ggcgggggaa	240
accccgctct	accctcactc	ctgaaagtat	gccttcacga	taagattgtc	aat	293

<210> 34
 <211> 633
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(633)
 <223> n = A,T,C or G

<400> 34						
atttacactt	tttacgaaat	catgggatca	ctaacaaaat	atcgcttgtc	agttatattg	60
tatggcagga	aagatatgcg	actgatatta	cagatcccca	aagtggagag	tttatgacca	120
ttaaaaataa	gatgttgctg	ggtgcgcttt	tgctggttac	cagtgccgcc	tgggccgcac	180
cagccaccgc	gggttcgacc	aatacctcgg	gaatttctaa	gtatgagtta	agtagtttca	240
ttgctgactt	taagcatttc	aaaccagggg	acaccgtacc	agaaatgtac	cgtaccgatg	300
agtacaacat	taagcagtgg	cagttgcgta	acctgcccgc	gcctgatgcc	gggacgcact	360
ggacctatat	gggtggcgcg	tacgtgttga	tcagcgacac	cgacggtaaa	atcattaaag	420
cctacgacgg	tgagattttt	tatcatcgct	aaaaaaagcc	ccctcatcat	gagggggaaa	480
tgacagacac	ttgntatttt	ttattattag	ccacttgctc	gtcttgcttg	gtattaagtc	540
gtatttcacg	ttgattaatg	cnggtggctc	cagtgcgcca	gattaacttt	gtttggatcg	600
aagacgtagt	aactggctgg	ttatcggaat	tgg			633

<210> 35
 <211> 569
 <212> DNA
 <213> E. Coli

<400> 35						
tatggcagga	aagatatgcg	actgatatta	cagatcccca	aagtggagag	tttatgacca	60
ttaaaaataa	gatgttgctg	ggtgcgcttt	tgctggttac	cagtgccgcc	tgggccgcac	120
cagccaccgc	gggttcgacc	aatacctcgg	gaatttctaa	gtatgagtta	agtagtttca	180
ttgctgactt	taagcatttc	aaaccagggg	acaccgtacc	agaaatgtac	cgtaccgatg	240
agtacaacat	taagcagtgg	cagttgcgta	acctgcccgc	gcctgatgcc	gggacgcact	300
ggacctatat	gggtggcgcg	tacgtgttga	tcagcgacac	cgacggtaaa	atcattaaag	360
cctacgacgg	tgagattttt	tatcatcgct	aaaaaaagcc	ccctcatcat	gagggggaaa	420
tgacagacac	ttgttatttt	ttattattag	ccacttgctc	gtcttgcttg	ttattagtcg	480
tatttcacgt	tgattaatgc	ggttgccctc	agtgcgccag	atttaacttt	gtttgtatcg	540
tagacgtagt	aactggctgg	tatcggaat				569

<210> 36
 <211> 338
 <212> DNA
 <213> E. Coli

<400> 36						
cgtattcaca	tccttttgat	tggtgataac	atgcgaatcg	gtattatttt	tccggttgta	60
atcttcatta	cagcggtcgt	atcttttagca	tggtttttta	ttggcggcta	tgctgccccg	120
ggagcataaa	gatgaaaaaa	acaacgatta	ttatgatggg	tgtggcgatt	attgtcgtac	180
tcggcactgc	ctgggatggg	ggtaacgtca	cctctaaaaa	atagcaaagg	ctgcctgtgt	240
gcagcctttg	tgcaatttaa	gcgttaactt	ttaatcttcc	tgtagataaa	tagcacgaca	300
atcgcaccaa	taacggcaac	cacgaagctg	ccaaaatt			338

<210> 37
 <211> 375
 <212> DNA
 <213> E. Coli

<400> 37
 ctgaatattt aaaaaggaaa acgacatgaa accgaagcac agaatcaaca ttctccaatc 60
 ataaaatatt tccgtggagc attttattat tgaatataga ggtttaactc cggtaaaaaa 120
 caaagaagca ttgaatgcag ggaaaaataa tatggccata aaaaacatcg aaagaaactc 180
 ttttaattta acatgtaaac gcatgggttaa tcctcatatc acgggtggag tgttaagaac 240
 atacataaat ggagtcattg tttccctttt ccatttatca agttcctgtt gccgttttag 300
 tccatctcta attgcatatt ttaatttttc tgataaatgg cattgagcat cgatttcatt 360
 taaaacaact gtaca 375

<210> 38
 <211> 446
 <212> DNA
 <213> E. Coli

<400> 38
 ttacgatagc tattagtaaa aatataagag ttagctgtat tggtatgtct gtggcgaaat 60
 tgactacctt cgtttttttg attaagaatg attttattat cgtaagtaaa attacatgaa 120
 tatttaaaaa ggaaaacgac atgaaaccga agcacagaat caacattctc caatcataaa 180
 atatttccgt ggagcatttt attattgaat atagagggtt aactccggtg aaaaacaaag 240
 aagcattgaa tgcagggaaa aataatatgg ccataaaaaa catcgaaaga aactctttta 300
 atttaacatg taaacgcatg gttaatcctc atatcacggg tggagtgtta agaacataca 360
 taaatggagt catgttttcc cttttccatt tatcaagttc ctggtgccgt tttagtcctt 420
 ctctaattgc atattttaat ttttct 446

<210> 39
 <211> 392
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(392)
 <223> n = A,T,C or G

<400> 39
 tcaccccggt gccgattttc aggcacacctg atttaactta gcacccgcaa cttaactaca 60
 ggaaaacaaa gagataaatg tctaatacctg atgcaaatcg agccgatttt ttaatcttta 120
 cggactttta cccgcctggt ttattaattg cactgtnatc cgggcgttcg cccgctttaa 180
 tcacaatagg ctgtgtagcc tgggcctgtt tctctttcac ccgcgccaga gcggcagcaa 240
 tcgcatcttt atctttggct gcagggtgaa cggctgcgct cttatgtcgt tcaaggcgag 300
 ccgctttttc gcgctccaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg 360
 cncgcttttc ttcttgacga atagccgcaa tt 392

<210> 40
 <211> 208
 <212> DNA
 <213> E. Coli

<400> 40
 taataacgct atctgcggat aaagcagaat aggtgggttaa cccagacat aaaccgagga 60
 aaataatggt attgtatttc ataattctatt gttccttagc gacagattgc tgtctgctgg 120
 ttcagtaagg taccaggaga aacttcagga agcttgact cgacaataca gtttgagttt 180

ttatctttgc cccatgaaac ctgtaatt

208

<210> 41

<211> 342

<212> DNA

<213> E. Coli

<400> 41

catcctcaat accgttaa	at gcaacccgaa	cccccgttgt	ccctttgctg	cattcactta	60
acgtaatctg aaaagggacg	gctggacttg	tgctaccggt	cgttggaaat	tgtctggcac	120
tgtttttttg gagatctacg	gtaaaattaa	gcgaatccga	tgagactgtg	cagccataat	180
cgaggacgcg cccgctaatt	ttaataacgc	tatctgcgga	taaagcagaa	taggtgggta	240
accccgagaca taaaccgagg	aaaataatgt	tattgtattt	cataatctat	tgttccttag	300
cgacagattg ctgtctgctg	gttcagtaag	gtaccaggag	aa		342

<210> 42

<211> 841

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(841)

<223> n = A,T,C or G

<400> 42

agattttactg ccaatttccg	gcagatcgga	aaggggttaa	ccatattgat	ccataaggggt	60
acgaatcacg gctataccgc	caggcatggc	ttgagccatg	gcattaaatt	ccgcaaattc	120
gggcgctgat tcttcccacg	cggttatttt	ggcacacacc	agatccagca	aggggttntc	180
aggatcggtg agcagcagat	gatctaccag	ttncagcgcc	tgggtgtatt	gntccttggt	240
ctgaataccc gnnagaaaag	gtgccacagc	anttagcttn	tctcctgctt	gcaagatgtc	300
tggcaatngc aatcattttt	tgcacttant	acgatgnaca	ncngtaaaga	aatcgnattt	360
ttntatgccg tcataacttt	acgtatgtan	cactttttgc	nattcnaaaa	aagaccattn	420
gctncaacac gtaaattna	ttgncccccna	catttanaac	ataaatgntt	aaaatttttc	480
ccccncnnan ttttaagntn	ttnanagaat	ngggaattac	ctgcttttna	atgnactcan	540
anttttttng naataattcc	tntatcnaaa	ctnnttttcn	cccaanagnc	nnccaaattn	600
cggttttntn nttnncnngg	cnttttttta	cccnanaann	tttattcaan	nccttttttg	660
tagnctatnt naagnggnc	ttnttnnatt	aactttccnn	ttggncaaat	tttggcnnat	720
ttttatatan aattntctta	tntcntaatt	tnggnanccc	cngatgnaan	tttatggngg	780
gantcccnnt ccctntttaa	tnnatgntct	gggntatttt	taaancctnn	attaannnnan	840
c					841

<210> 43

<211> 215

<212> DNA

<213> E. Coli

<400> 43

aataactttt cgtaggcag	ttttgggtgt	gagttgcaag	aggggagact	actgaataac	60
tcaagtttta taatcgagg	gaaaatgggtg	atggcggttca	tagcaaaaacg	ccctcaacca	120
taaaggtcga gggcgcttaa	gatgttaaaa	acccgctatc	cgttaaaaaaa	caatgttcaa	180
ctaaggtcag tgacattg	cg ctaaaaaagc	gaatt			215

<210> 44

<211> 395

<212> DNA

<213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(395)
 <223> n = A,T,C or G

<400> 44
 gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttgttat 60
 ttaagggttta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg 120
 gcattgctat aatattgggt atcatttgct gaatggattc agtcttaatg agtggggttt 180
 taagggacag gcatagagta atgatacgta tgcataacca acatctttac tcattatgtc 240
 attgaatgtt gaccctatgt gtttatgaag gagaggattt ttcagttgat ctggattgnt 300
 aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa 360
 atattgaaat agtccaacta cttctttatt accaa 395

<210> 45
 <211> 883
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(883)
 <223> n = A,T,C or G

<400> 45
 ataatcaggt aagaaaaggt ggcgcggagat taccgtgtgt tgcgatatat tttttagttt 60
 cgcggtggcaa tacatcagtg gcaataaaaac gacatatcca gaaaaatata cactaagtga 120
 atgatatctt ccgattttatc ttaatcgttt atggataacg gcaaagggtc tcgttttttc 180
 ctatacttat tcagcactca caaataaagg aacgccaatg aaaattatac tctgggctgt 240
 attgattatt ttctgtattg ggctactggg ggtgactggc gtatttaaga tgatatttta 300
 aaattaatta atgtcatcag gtccgaaaat aacgagaata tttcagtctc tcacccctgtt 360
 gcgctcctgt catgtgcatt gcttcatata atcactggcg caaggagcgc cgcaggcgna 420
 gnntgcnngn cgnccacct naccatgc cgaacttcag aantgaaaac nccntaacnc 480
 cgatngtcgg cggnggcctc cccatgcnan agtangggaa ntgccangcg ncnntataaa 540
 cgaaaggctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc 600
 tcttgagnan gacaaatncc gccgggagcg gatttgaacn ttgcgaagca accgncnna 660
 agggngnngt cntgacnccc nncctctant nnngccttc ttttgcttna angncctcct 720
 ancngatggc ctttttngcc ntctaccaa cnntttggtt aatgcttnta aaancctttc 780
 canntncaa tccngtnntn cccatccnnn tnttgaaagn ntncctnccn tgncantnt 840
 anntnngggg gnnngnggcc ggcggncccc ccccccccc ccc 883

<210> 46
 <211> 1024
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(1024)
 <223> n = A,T,C or G

<400> 46
 gtttatggat aacggcaaaag ggcttcgttt tttcctatac ttattcagca ctcacaaata 60
 aaggaacgcc aatgaaaatt atactctggg ctgtattgat tattttcctg attgggctac 120
 tgggtggtgac tggcgtatct aagatgatat tttaaaatta attaattgtca tcagggtccga 180
 aaataacgag aatatttcag tctctcatcc tgttgcgctc ctgtcatgtg cattgcttca 240

tataatcact	ggcgcaagga	gcgcgcagag	tntccnant	nnnnntnntt	ntntnctnn	300
nccttcacna	tncnncncn	nantnnatag	nnccacnntn	ttnttcnnnn	gnccnctcc	360
nnncnnnnnn	ncatnnnate	ccactnnntt	tntccannn	nnncnnnntn	cancncaaa	420
antncnaccn	anntnacctt	atacnnannc	nancnnnnnn	nnccactctn	netcgnnctc	480
cccnttcnac	nnccannnnn	cancnntcnn	ctnnnnccct	nnentaattn	ttctnnctan	540
ntectanccn	cnnacnnncc	cancnatccn	nnnatacant	cnattntntn	cnntcncntn	600
cncnnttcc	nnctnnncnc	tnccncatnc	ccnnnannan	canntncccc	ncctnccctna	660
ccnncnncnc	ccnccatccc	nncccnncnt	ccnnantnga	caannnnaat	cncnnnnncn	720
nnnnnnnnnn	tnnnncnccn	gcncnncnt	ncntcacnc	tnnncncta	nannnnntac	780
nntnaccnnt	cctnnacnc	tnccctnnng	antccnacna	ntnnnnnanc	nanaacnctn	840
tnnnnccata	atcccacacc	acncccntnc	ancntntnt	ncntcntccc	ttcntatcnc	900
agctnnnnnt	ncntntnnnc	tnccncccn	cnnactncnn	nnaccnncnn	cccantcagt	960
ccacntccn	cnnnnnnntn	nnncnancn	ctnnacnncn	cnantaacct	nntnncacct	1020
tccc						1024

<210> 47
 <211> 236
 <212> DNA
 <213> E. Coli

<400> 47						
atatacacta	agtgaatgat	atcttccgat	ttatcttaat	cgtttatgga	taacggcaaaa	60
gggcttcgtt	tttccctata	cttattcagc	actcaciaat	aaaggaacgc	caatgaaaat	120
tatactctgg	gctgtattga	ttattttcct	gattgggcta	ctgggtgtga	ctggcgtatt	180
taagatgata	ttttaaaatt	aattaatgtc	atcaggtccg	aaaataacga	gaatat	236

<210> 48
 <211> 418
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(418)
 <223> n = A,T,C or G

<400> 48						
cggagattac	cgtgtgttgc	gatataat	ttagtttcgc	gtggcaatac	atcagtggca	60
ataaaacgac	atatccagaa	aaatatacac	taagtgaatg	atatcttccg	attnatctta	120
ntcgtttatg	gataacggca	aagggcttcg	tttttcccta	tacttattca	gcactcacia	180
ataaaggaa	gccaatgaaa	attatactct	gggctgtatt	gattattttc	ctgattgggc	240
tactggtggt	gactggcgta	tttaagatga	tattttaaaa	ttaattaatg	tcacagagtc	300
cgaaaataac	gagaatat	cagtctctca	tcctgttgcg	ctcctgtcat	gtgcattgct	360
tcataataatc	actggcgcaa	ggagcgcgca	ngggcgggcc	aatcgccgcc	ggcccctg	418

<210> 49
 <211> 550
 <212> DNA
 <213> E. Coli

<400> 49						
ctgctagtta	caggggaacac	taatgacaga	cagctaaaag	ccctgtttta	ttacgtatta	60
caaacagggg	atgccagcgc	ttttcgtgca	tttattggtg	agatagcgga	acgcgcacca	120
caagaaaagg	agaaactgat	gaccattgct	gacagattac	gtgaagaagg	cgcaatgcag	180
ggcaaacacg	aagaagccct	gcgtattgct	caggagatgc	tggatagagg	tttagacaga	240
gagttagtta	tgatggtgac	ccgactttca	ccagacgatc	ttatcgcgca	aagccactaa	300
tcctgtaaca	ccgggaggtta	actggcggat	gtttgctgta	aaccacatca	gcgaacgaca	360

tccgccagcg	cctcttctaa	atcgtaggag	cgaaacgcaa	aacccgcttc	ttccagccgt	420
ttaggcagcg	cgcggtgtcc	acctaatacc	agtactgaag	attcgcccat	taacagtcga	480
atggcggtcg	cggggacgcg	caaaatggcc	gggcgatgca	gcgcgatgacc	gagcgcatgg	540
gcaaattggt						550

<210> 50
 <211> 99
 <212> DNA
 <213> E. Coli

<400> 50						
ttggcatctc	ggtgttgccg	atcttcatga	tatccagccc	gccggaaact	tcttcccaaa	60
cggttttgct	ggtatccatt	gagtcacgga	actgcccct			99

<210> 51
 <211> 259
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(259)
 <223> n = A,T,C or G

<400> 51						
ccgtgccgag	atgatcctgt	naccatcatc	cgttgtgaag	tagtgattca	cgacttcaag	60
gcgcttttca	aaaggggtatt	ttggctttga	catattaggg	gctattccat	ttcatcgnc	120
aacaaaatgg	gtgcagtaca	tactcnttgg	aaatcaacac	aggaggctgg	gaatgccgca	180
gaaatataga	ttacttttctt	taatagtgat	ntgtttcacg	cttttatttt	tnaaanaagt	240
tnggcttact	tcccggggn					259

<210> 52
 <211> 877
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(877)
 <223> n = A,T,C or G

<400> 52						
cagcagagcg	cgcccttctt	cgtagatttt	cgtagtagtg	gtaatggtaa	tatccaaacc	60
acgaacgcgg	tcgactttat	cgtagtcgat	ttctgggaag	atgatctgct	cacggacacc	120
catgctgtag	ttaccacgac	cgtagaaaga	cttagcggac	aggccacgga	agtcacggat	180
acgaggtaca	gcaatagtga	tcaggcgctc	aaagaactcc	cacatgcgtt	cgccacgcag	240
agttacttta	cagccgatcg	gatagccctg	acggattttg	aagcctgcaa	cagatttgcg	300
tgctttggtg	atcagcggtt	tttgaccgga	gattgctgcc	aggtctgctg	ctgcgttata	360
cagcagtttt	ttgtcagcga	tcgcttcacc	aacacccatg	ttcagggtga	tcttctcgac	420
ccgagggact	tgcatgacag	aattgtagtt	aaactcagtc	atgagttttt	taactacttc	480
gtctttgtag	taatcatgca	gtttcgccat	cgtactactc	catgtcgggtg	aacgctctcc	540
tgagtaggac	aaatccgcgg	ggagcggatt	tgaacgttgc	gaagcaacgg	cccggagggt	600
ggcgggcagg	acgcccgcga	taaactgcca	ggcatcaaat	taagcagaag	gccatcctga	660
cggatggcct	ttttgcgttt	ctacaaaactc	ttttggttat	ttttctaaat	cattcaaata	720
tgtatccgnt	catcccatcc	tatcgatgat	aagctgtcaa	acatgagaat	ttaatcaatc	780
taaagtttta	tgnggttaaa	cttgggctgg	cagnttncca	atggcttaat	cagtnagagg	840
ccctatntta	acgaactngg	ctantttngg	tcaatcn			877

<210> 53
 <211> 291
 <212> DNA
 <213> E. Coli

<400> 53
 tgaacagcag agatacggcc agtgcggcca atgttttttg tccttttaaac ataacagagt 60
 cctttaagga tatagaatag gggatatagct acgccagaat atcgtatttg attattgcta 120
 gtttttagtt ttgcttaaaa atattgtag ttttattaaa tgcaaaacta aattattggg 180
 atcatgaatt tgttgtaga tgaataaaa ataggggggt atagatagac gtcattttca 240
 taggggtata aatgcgacta ccatgaagtt ttttaattgaa agtattgggt t 291

<210> 54
 <211> 282
 <212> DNA
 <213> E. Coli

<400> 54
 ttattaaatg caaaactaaa ttattggtat catgaatttg ttgtatgatg aataaaatat 60
 aggggggtat agatagacgt cattttcata ggggtataaa tgcgactacc atgaagtttt 120
 taattgaaag tattgggttg ctgataattt gagctgttct attcttttta aatatctata 180
 taggtctgtt aatggatttt atttttacaa ttttttgtt ttaggcatat aaaaatcaac 240
 ccgccatatg aacggcgggt taaaatattt acaacttagc aa 282

<210> 55
 <211> 293
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(293)
 <223> n = A,T,C or G

<400> 55
 cggggtccgg cgctcatcaa caatcggggg gcagcaagg gctgaaacgg gaaagcccct 60
 cccgaagaag gggccttgta taaggaaagg gttatgatga agctcgtcac catactggtt 120
 gtgtngttac tgtaagttt cccgacttac taacaactca tcagaggggg gagaaatcct 180
 cccttaccct tgttccttta ctctagggtt aaaaaacaac agcgtcaata ggcctgccat 240
 gtacgaagcg agatctgtga accgctttcc ggtagcctt ttttatcctg ttg 293

<210> 56
 <211> 300
 <212> DNA
 <213> E. Coli

<400> 56
 tctgcgttcc gctaaaagg gcaaatgctc aggacgttgc agcgttttgc gtgaccgctc 60
 ggggaaggca aaattgcctc tgggaaagca ttgcgcgggg tccggcgctc atcaacaatc 120
 ggggggcagc aaggggctga aacgggaaag cccctcccga agaaggggcc ttgtataagg 180
 aaagggttat gatgaagctc gtcacatac tggttggtt gttactgtta agtttcccga 240
 cttactaaca actcatcaga ggggggagaa atcctccctt acccttgctc ctttactcta 300

<210> 57
 <211> 359
 <212> DNA

<213> E. Coli

<400> 57

caacacagga	ggctgggaat	gccgcagaaa	tatagattac	tttctttaat	agtgatttgt	60
ttcacgcttt	tatttttcac	ctggatgata	agagattcac	tgtgtgaatt	gcattattaaa	120
caggagagtt	atgagctggc	ggcgttttta	gcctgcaaat	tgaaagagta	agagtcttcg	180
gcgggaaatt	attcccgcct	tacttacggc	gttgcgcat	ctcattgcac	ccaaatttat	240
tcttcacaaa	aataataata	gattttatta	cgcgatcgat	tatttatttc	ctgaaaacaa	300
ataaaaaaat	ccccgccaaa	tggcagggat	cttagattct	gtgcttttaa	gcagagatt	359

<210> 58

<211> 700

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(700)

<223> n = A,T,C or G

<400> 58

aaaccttttt	ctctgtttt	tcatagaggg	caacccatgt	cctgacctgg	gttcggggga	60
cacaaaaacg	tgccgagatg	atcctgtaac	catcatcagt	tgtgaagtag	tgattcacga	120
cttcaaggcg	cttttcaaaa	gggtattttg	gctttgacat	attaggggct	attccatttc	180
atcgtccaac	aaaatgggtg	cagtacatac	tcgttggaat	tcaacacagg	aggctgggaa	240
tgccgcagaa	atatagatta	ctttctttta	tagtgatttg	tttcacgctt	ttatttttca	300
cctggatgat	aagagattca	ctgtgtgaat	tgcataatga	acaggagagt	tatgagctgg	360
cggcgttttt	agcctgcaaa	ttgaaagagt	aagagtcttc	ggcgggaaat	tattcccgcc	420
ttacttacgg	cggtgcgcat	tctcattgca	cccaaattta	ttcttcacaa	aaataataat	480
agatttttatt	acgcgatcga	ttattttatt	cctgaaaaca	aataanaaaa	tccccgccaa	540
atggcaggga	tcttagattc	tgtgctttta	agcagagatt	acaggctggg	tacgttacca	600
gctgcccggc	ctttaacgcc	gctttcgatg	gtgaaggaca	ctttctgacc	ttcgtccaga	660
gattgtaacc	atcgggtctg	atagccnaga	aatgtccaac			700

<210> 59

<211> 631

<212> DNA

<213> E. Coli

<220>

<221> misc_feature

<222> (1)...(631)

<223> n = A,T,C or G

<400> 59

tggtggcatt	ggttgctgga	gagagaaaaa	ccccgcacgt	tgcaggatat	cacctgacaa	60
caccacgggg	gctaattctg	actctagacc	actcaagaat	agccgcgaaa	cgttgtcatt	120
acaacacagg	cggctatatg	acgttcgcag	agctgggcat	ggccttcttg	catgatttag	180
cggctccggg	cattgctggc	attcttgcca	gtatgatcgt	gaactggctg	aacaagcgga	240
agtaacgtgt	catgcgggcg	tcaggctgcc	gtaatggcaa	tttgcgcccg	gaccaggccg	300
caggggggaa	actctgcggc	ctttttcggt	cttactgcgg	gtaaggcacc	cagtcgccgc	360
cgttcaggcg	aacgtacggg	ttatcctggg	attgaataac	tactgcattt	gagttctcgg	420
agaccgggtg	tgtttgtggc	aacccactgg	tgagtttttt	ccagtcaaca	ttgtcttcgg	480
tgaaaatcct	gccatcgaga	acgcgaacca	ccagatcgga	gatagccagg	aagctgctcg	540
gttggtcgat	gacaatcggg	gccccctgat	gcgggtgcct	catgccgaag	aatttcaccc	600
caacggggac	gtcngtgata	gaccggggcta	g			631

<210> 60
 <211> 648
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

```

<400> 60
ggctcaggcn tgctgattgt ttttttgtgc aatggcccng tattagcgtc gttgctgtcg      60
atggagagaa tcataaacgt ggtgaatgat gattgttagc aaggaaaact gtcaaaaatc      120
ttcaaaaaat ttgagggata aggccggaat ggctccggcc agagggaagt taaccgcgaa      180
gctgttgctg cttgagggtc gttttaacca gacgccaggc gctccatacg ccaaaaccgc      240
gtctggccca gcggaccagc atattaggat ggcgaaatcgt ccagatcgcc atcacgctac      300
tgccaaccag cgcccaggag cgcgacttta gcagcatatt ccancgacga tcgtaagcgc      360
ctgttgcttc cagccattca cgcgacttgg cggaagggnc cgcgctgac caacttgct      420
tttagctga tncanattan attnataaac gcagnanncn ggtntgatta atcntatttn      480
gctctngtct ggtagttagc nncggnnngt ctcnttntna cccnnttcnn tttannttac      540
natnngtaan ttatntttnt nngtctnant tntanttgng tactntaagt ntatncgnnn      600
atnntnnnan nnnncagnnc ntntttttta aatnntttnt nanncnnc      648
  
```

<210> 61
 <211> 737
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(737)
 <223> n = A,T,C or G

```

<400> 61
tgctaataatc tttctcattg agatgaaaat taaggtaagc gaggaaacac accacaccat      60
aaacggaggc aaataatgct gggtaatatg aatgttttta tggccgtact gggaataatt      120
ttattttctg gttttctggc cgcgtatttc agccacaaat gggatgacta atgaacggag      180
ataatccctc acctaaccgg ccccttggtta cagttgtgta caaggggcct gatttttatg      240
acggcgaaaa aaaaccgcca gtaaaccggc ggtgaatgct tgcattgata gatttgtgtt      300
ttgcttttac gctaacaggc attttcctgc actgataacg aatcgttgac acagtagcat      360
cagttttctc aatgaatgtt aaacggagct taaactcggc taatcacatt ttgttcgtca      420
ataaacatgc agcgatttct tccggtttgc ttacctcat acattgcccg gtccgctctt      480
ccaatgacca catccagagg ctcttcagga aatgcgcgac tcacacctgc tgtcacggta      540
atgttgatat gcccttcaga atgtgtgatg gcatggttat cgactaactg gcaaattctg      600
acacctgcac gacatgcttc ttcatcatta gccgctttga caataatgat aaattcttcg      660
cccccgtagc gataaaccgt ttcgtaatna cgcgtccaac tgggntaagt aaagttgcca      720
gggtgccgta atcttac                                     737
  
```

<210> 62
 <211> 648
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(648)
 <223> n = A,T,C or G

```

<400> 62
tgcttttgaa tatgtgctcg caatcttgag aaggaaatgg cgaccacgaa agaaaaggca      60
aaaaccgata atctgaaaga acccaagtat ttcagtataa gcattgaatg ccgaccagta      120
aactctttcg gattcaccga gaaagtgaan ccaaaatgat aatcgtatac ataagtcttt      180
cgagtggctc gttagcaaaa agtttcaaca atggagtaaa tacatccaac atatcaataa      240
ctctcaactg taaggggatt gaaatggtaa cccagctctc tcgcttgagg ggtatagccg      300
agaccaccga agccccggag gtggtgaaat aaaaccgggc acaacacgaa agggcgcatc      360
tccgatatcc ataaaagaag tcgggtcttt gtctggtaaa attaaattgg tgggaagtgc      420
gcctccgggt tgtaaatacc gactttgctg ggtgtagcct ggcggcatca agtttttttc      480
tggaagtctg ctgatgtccg ccttttttaa agggaatttt ggtgatgccg gtgaatgccg      540
cttaaccccc cgtgggcccc gttaaaagtc atggtaagnc ctaatnggtt tgggggtggga      600
aaagccnact gnnaattggt tacctggttt gcaagtancc ctggaagg      648

```

```

<210> 63
<211> 237
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(237)
<223> n = A,T,C or G

```

```

<400> 63
ggtgtttant tacaagagat tcctctttgt ntaaancccn gataagtaat tacgcataaa      60
acaacaatga ttataatagc aaaaataaat attatcatct ttgatagatt acttgagata      120
gccagcatct tgtaaagcct ttatcgtttt tttatgctct ggattaatat aatcactaca      180
tctatctgag caatctgttg ttgatggaca tgtcaacca tggtcattta cagccaa      237

```

```

<210> 64
<211> 427
<212> DNA
<213> E. Coli

```

```

<400> 64
gataattaga gtttgtcgtc agaaaattga cgttacccat aacaaatgaa aggccaggta      60
aatcatgccca ttagtcattg ttgctatcgg tgtaatcttg ttgttgctcc tgatgatccg      120
cttcaaaaatg aacggcttca tcgctctcgt cctcgtggcg cttgctgttg gattaatgca      180
aggaatgccg ctggataaag ttattggctc catcaaagcc ggtgtcggcg ggacgctcgg      240
tagccttgcc ctgatcatgg gttttggcgc aatgctgggc aaaatgctgg cagactgcgg      300
tggcgacaaa cgtatcgcca ccacgctgat tgccaaattt ggtaaaaaaac acatccagtg      360
ggcggtggtg ctgaccggtt ttaccgttgg ttttgccctg ttctatgaag tgggctttgt      420
gctgatg      427

```

```

<210> 65
<211> 261
<212> DNA
<213> E. Coli

```

```

<220>
<221> misc_feature
<222> (1)...(261)
<223> n = A,T,C or G

```

```

<400> 65
caaagaacct tcaacatgaa aaatatccat ttgtttgcaa aaaaagatta ttaggaagga      60

```


aattaatgca attatcgaaa attcaaaaaa tatccaaaaa tngtatactt tattccagaa	120
gagttcaata taatgtttgt cttcaatfff tcttacttca gggtaatata gattgctcat	180
tacattgtga gcttcatctt tatttaatff tctgttgact ccagctctcc gtgataacgg	240
ttttataatt agatgcttat c	261

<210> 66
 <211> 98
 <212> DNA
 <213> E. Coli

<400> 66	
agatgattgc cgggaacttg ttagcggcac gcaggcggcg gctcgcaccc ttaccctgct	60
ctttacgtac ttctgcgttg atagtaaaca tttctttc	98

<210> 67
 <211> 260
 <212> DNA
 <213> E. Coli

<400> 67	
aagcgcgaac gaagtcgatg tgctgcagct tcggtttgta cgggtgacgc tgtacgtcct	60
gagctttaac tttgatttct ttaccgtcaa caacgatggc cagaacttcg ctgtagaatt	120
cagcttttagc ttgcatgttc atgactttgt cgtgatccag ctcgatagcc agcggcgctt	180
ctttgccacc gtagatgatt gccgggaact tgtttagcggc acgcaggcgg cggctcgcac	240
ccttaccctg ctctttacgt	260

<210> 68
 <211> 95
 <212> DNA
 <213> E. Coli

<400> 68	
aaaaacggcg taaagaaagg ttgcaaacat gttaataaaa actcaaattg atcccacgta	60
tatattacgc cgcaaaatcc ttacaataaa caggg	95

<210> 69
 <211> 174
 <212> DNA
 <213> E. Coli

<400> 69	
ttaattatta aaatagtgtg acgcgattat gtggttatgg gggtaaacad taaataaacc	60
agcggggagg ggaggtaaag tgaaaaaata aaaagcggat aatcttaata agcaggccgg	120
acagcatcgc catccggcac tgatacgagg tttatttcag ctcatcaacc atcg	174

<210> 70
 <211> 138
 <212> DNA
 <213> E. Coli

<400> 70	
agtctgtaaa aacgtcaaaa agagtgtttt atcaacagaa gaatggaggc ctgacagata	60
gtagtaatgc aaaaaaatgg agacttaagt tgaatgaacg ggagtaaagc gaaaagacta	120
tagagtgaag gagaaatt	138

<210> 71
 <211> 191

<212> DNA
 <213> E. Coli

<400> 71
 tttgttggct taatattcta ttgttatctt tatttataga tgtttatatt gcatgaggtg 60
 gtttttggag agaagaatga ggaagatgcg tcgagccaca gaaacgtag ctttacatat 120
 agcggaggtg atgtgaattt aatttacaat agaaataatt tacatatcaa acagtttagat 180
 gctttttgtc g 191

<210> 72
 <211> 244
 <212> DNA
 <213> E. Coli

<400> 72
 ggccatttat acaggaaaag cctatgtcag aacgtaaaaa ctcaaaatca cgccgtaatt 60
 atctcgtaa atgttcctgc ccaaactgca cccaagagtc agaacacagt ttttcaagag 120
 tacaaaaagg tgcccttttg atctgccctc attgcaacaa agtattccag acaaacttta 180
 aagctgtagc ctgattgatt ttattagtaa caagtatttt ttatatttta ataatatatt 240
 taaa 244

<210> 73
 <211> 327
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 73
 aaattttcag gtaccttgtc accatacttt tttttctgag cattaatgat attttgagct 60
 tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaaggntg 120
 aataatttgn ctttataaat cgccagtgga gaattagtaa aacgattaaa ttctactaaa 180
 tnattaaccg naaaaaaatt cccatatata tttatcattg gtatgaaaaa tatgtgcacc 240
 atatttatga atntggatac cctnacagtc ctctgtgtac gcatttccac cgatatgatt 300
 tcttttctna atcactaaaa ctttttt 327

<210> 74
 <211> 150
 <212> DNA
 <213> E. Coli

<400> 74
 gcagtgatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
 tgactttcgc cggacgtcag gccgccactt cgggtgcggtt acgtccgggt ttttttgcgt 120
 tgtaaagcgc caaatctgcc gatttcaacc 150

<210> 75
 <211> 330
 <212> DNA
 <213> E. Coli

<400> 75
 gaaagtatct tcgttattga catcaactgga aaatataact tgcttttcat tattaaactc 60
 gaagcgcgta ccgtatctgg acaaacattt atcgagctta ccaaatcct gaagaggttt 120

aactacagat	aacatttgcg	cgtcctttgc	agtaatgccc	gtcaaatacct	tgacggggcat	180
tatttagatt	aaattaccag	tatttcttcg	gagtgaagaa	tattaccagg	tatatttaac	240
acccacgttc	gcggaccagt	cttgatctac	gtcaccacca	ccgaggtagt	tagcatcggt	300
ataggcgctg	aagttcttgg	tgaagctaaa				330

<210> 76
 <211> 194
 <212> DNA
 <213> E. Coli

<400> 76						
tgtttttttc	cagcaacgga	gcaaaaagggt	tgcccttgtg	cagctcaggg	ttaaccactt	60
taactacgtg	gcgacgaccc	ggagatgtcg	gtttacattt	aacaactgcc	attgtattac	120
tcctccgact	tactcagcgc	cgccaacgaa	gtccagattc	tggccttctt	tcagggtgac	180
gtaagctttt	ttcc					194

<210> 77
 <211> 188
 <212> DNA
 <213> E. Coli

<400> 77						
tccctttaac	taccaggggtg	ttaacgactt	cgacttcgac	ttcaaacagt	ttctgcacag	60
cagctttgat	ttctgctttg	gtcgcgtctt	tagcaacttt	gagtactatg	gtgttggtt	120
tttccatcgc	agtagacgct	ttttcagaaa	cgtgcggtgc	acgcagcacc	ttcagcagac	180
gttcttca						188

<210> 78
 <211> 173
 <212> DNA
 <213> E. Coli

<400> 78						
acaaaggcga	acaaagcctg	tgaagcccga	aggctccaca	gacagtgcta	cttgaaggcc	60
ttactgtttc	ttcttaggag	cgagcaccat	gatcatctgg	cggccttcga	tcttggttgg	120
gaaggattcg	accactgcc	gttcttgcaa	atcgtctttc	acgcgattaa	gca	173

<210> 79
 <211> 272
 <212> DNA
 <213> E. Coli

<220>
 <221> misc_feature
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 <223> n = A,T,C or G

<400> 79						
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aaagaagaca	ctactcttag	ccctttaaca	tttaacgcat	tgtcacgaac	tcttctgccg	180
ccgttgggtg	aatggcgacg	ggtattggtc	gaaatctttt	ttgggtggcc	ccatctttaa	240
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<210> 80
 <211> 259
 <212> DNA

<213> E. Coli

<400> 80

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aacaccgata	accattgagt	tcagcagggc	acgcgcggta	ccagcctgtg	cccaaccgtc	180
tgcgtaacca	tcacgcggac	cgaaggtcag	ggtattatct	gcattgttta	cttcaacagc	240
atcggtgaga	gtacgagtc					259

<210> 81

<211> 73

<212> DNA

<213> E. Coli

<400> 81

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ccgtttaccg	ggg					73

<210> 82

<211> 666

<212> DNA

<213> E. Coli

<400> 82

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gtcgattact	gtttcaaagt	gttaatcagt	atcgttttct	tcctgccaat	gtatggcgta	600
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agttaa						666

<210> 83

<211> 612

<212> DNA

<213> E. Coli

<400> 83

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gttattcagt	aa					612

<210> 84

<211> 975

<212> DNA
 <213> E. Coli

<400> 84

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gctgccgggg	actcactgga	taaagcaacg	ttgaaaaagg	ttgcgccgaa	gcctggctgg	180
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<210> 85
 <211> 1761
 <212> DNA
 <213> E. Coli

<400> 85

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atcgcgcaag	catcgcaaca	ggaaggacgt	caccgttttc	catggccatt	acgttggtcg	1740

aactggttta ttccgaactg a

1761

<210> 86

<211> 1185

<212> DNA

<213> E. Coli

<400> 86

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<210> 87

<211> 2115

<212> DNA

<213> E. Coli

<400> 87

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 <211> 540
 <212> DNA
 <213> E. Coli

<400> 88						
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<210> 89
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 <212> DNA
 <213> E. Coli

<400> 89						
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<210> 90

<211> 375

<212> DNA

<213> E. Coli

<400> 90

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<210> 91

<211> 366

<212> DNA

<213> E. Coli

<400> 91

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aaataa						366

<210> 92

<211> 498

<212> DNA

<213> E. Coli

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<210> 93

<211> 2145

<212> DNA

<213> E. Coli

<400> 93

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<210> 94

<211> 1767

<212> DNA

<213> E. Coli

<400> 94

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<210> 95
 <211> 1227
 <212> DNA
 <213> E. Coli

<400> 95						
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<210> 96
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 <212> DNA
 <213> E. Coli

<400> 96						
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<210> 97
 <211> 771
 <212> DNA
 <213> E. Coli

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 <213> E. Coli

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<210> 99
 <211> 1536
 <212> DNA
 <213> E. Coli

<400> 99						
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 <211> 1029
 <212> DNA
 <213> E. Coli

<400> 100						
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<210> 102
 <211> 1023
 <212> DNA
 <213> E. Coli

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<210> 103
 <211> 876
 <212> DNA
 <213> E. Coli

<400> 103

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<210> 104

<211> 291

<212> DNA

<213> E. Coli

<400> 104

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<210> 105

<211> 1152

<212> DNA

<213> E. Coli

<400> 105

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<210> 106
 <211> 3048
 <212> DNA
 <213> E. Coli

<400> 106

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 <211> 885
 <212> DNA
 <213> E. Coli

<400> 107

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<210> 108
 <211> 654
 <212> DNA
 <213> E. Coli

<400> 108

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<210> 109
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 109

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<210> 110
 <211> 1203
 <212> DNA
 <213> E. Coli

<400> 110

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<210> 111

<211> 1179

<212> DNA

<213> E. Coli

<400> 111

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<210> 112

<211> 1326

<212> DNA

<213> E. Coli

<400> 112

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<210> 113

<211> 585

<212> DNA

<213> E. Coli

<400> 113

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ggcggtaacg	atgacagctc	atggctaccg	ctacttcacg	acctgacgaa	cgaaggcatg	180
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acgcaaccga	agctggataa	agtgaccggc	gaaaccggtg	aagctatcga	cgatctgcgt	420
aacattgcgc	aactgggtta	cgacgaagac	gaagatcagg	aagagcttga	aatgtcgcctt	480
gaagagatca	tcgaatacgt	tcgtgttgcc	gcgctgttat	gccacgacac	ctttactcat	540
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<210> 114

<211> 363

<212> DNA

<213> E. Coli

<400> 114

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ggtttcggtt	tggctgtgag	ctttagcttc	ttcgcgaatg	caaaattcac	attcaaggca	180
tcgactacaa	cgatgcgcta	catgctatat	gttgggttca	tggggacact	gagtgtact	240
gttggtatggg	ctgctgatag	atgcgcactt	ccccgatga	taactcttgt	caccttctcc	300
gccatcagcc	tgggtgtgcgg	tttcgtctat	tcaaagttca	ttgtcttttag	ggatgcgaaa	360
tga						363

<210> 115

<211> 921

<212> DNA
<213> E. Coli

<400> 115

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aaaacggtac	gtgaattcga	agaattgaag	tcatatgaag	tggaaatcgt	tttcataaat	120
gacggcagca	aagacgctac	ggagtcaatc	attaatgctc	tggctgtttc	agatcctcta	180
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gaccatgcaa	ccggggatgc	gataatccca	attgatgttg	acctgcaaga	cccgattgag	300
gttattcctc	atcttattga	aaaatggcaa	gcagggtgctg	atatggttct	tgctaaaaga	360
tctgaccgct	caactgatgg	acgcctgaag	cgaaaaacgg	ctgagtgggt	ctataagctc	420
cacaataaaa	taagcaatcc	taaaattgaa	gagaatggtg	gtgatttcag	gctgatgagc	480
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<210> 116
<211> 1332
<212> DNA
<213> E. Coli

<400> 116

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gtaatatata	tttattcatt	atatgcgata	tttacttcat	atataaaaaac	agaaagggtat	360
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gtaaagcact	aa					1332

<210> 117
<211> 249
<212> DNA
<213> E. Coli

<400> 117

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atgccaggta	aagatggagg	tggattcttt	atgactatcc	tgctggggat	agtcgggtgcc	120
gtagtcggcg	gatggatcag	cacgctgttt	ggctttggta	aagtcgatgg	cttcaatttt	180
ggcagcttcg	tggttgccgt	tattggtgcg	attgtcgtgc	tatttatcta	caggaagatt	240
aaaagttaa						249

<210> 118
 <211> 183
 <212> DNA
 <213> E. Coli

<400> 118						
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tatgaaacag	agacgccgat	gactttgctg	gtgccagaag	tgccggctga	agtataaaaa	120
gatctggtga	ataccgtacg	ttcttatgac	acggaaaacg	aacatgatgt	ttgtggttgg	180
taa						183

<210> 119
 <211> 360
 <212> DNA
 <213> E. Coli

<400> 119						
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<210> 120
 <211> 741
 <212> DNA
 <213> E. Coli

<400> 120						
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<210> 121
 <211> 1395
 <212> DNA
 <213> E. Coli

<400> 121						
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<210> 122

<211> 3123

<212> DNA

<213> E. Coli

<400> 122

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<210> 123

<211> 3078

<212> DNA

<213> E. Coli

<400> 123

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<210> 124

<211> 1416

<212> DNA

<213> E. Coli

<400> 124

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<210> 125
 <211> 1035
 <212> DNA
 <213> E. Coli

<400> 125						
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<210> 126
 <211> 2481
 <212> DNA
 <213> E. Coli

<400> 126						
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 <211> 720
 <212> DNA
 <213> E. Coli

<400> 127						
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<210> 128
 <211> 543
 <212> DNA
 <213> E. Coli

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taa						543

<210> 129

<211> 339
 <212> DNA
 <213> E. Coli

<400> 129

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<210> 130
 <211> 582
 <212> DNA
 <213> E. Coli

<400> 130

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<210> 131
 <211> 579
 <212> DNA
 <213> E. Coli

<400> 131

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<210> 132
 <211> 2223
 <212> DNA
 <213> E. Coli

<400> 132

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<210> 133

<211> 1059

<212> DNA

<213> E. Coli

<400> 133

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1059

<210> 134

<211> 621

<212> DNA

<213> E. Coli

<400> 134

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<210> 135

<211> 696

<212> DNA

<213> E. Coli

<400> 135

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gcaggaaaat	acctgattga	tgaaagaatg	aaaaagcgcc	gtgctgaagc	agctgcagaa		660
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<210> 136

<211> 636

<212> DNA

<213> E. Coli

<400> 136

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<210> 137
 <211> 504
 <212> DNA
 <213> E. Coli

<400> 137

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<210> 138
 <211> 531
 <212> DNA
 <213> E. Coli

<400> 138

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<210> 139
 <211> 1149
 <212> DNA
 <213> E. Coli

<400> 139

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<210> 140
 <211> 417
 <212> DNA
 <213> E. Coli

<400> 140

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<210> 141
 <211> 315
 <212> DNA
 <213> E. Coli

<400> 141

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<210> 142
 <211> 7152
 <212> DNA
 <213> E. Coli

<400> 142

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<210> 143

<211> 186

<212> DNA

<213> E. Coli

<400> 143

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gtatcattac	tctatgcctg	tcccttaaaa	accactcat	taagactgaa	tccattcagc	180
aatga						186

<210> 144

<211> 1197

<212> DNA

<213> E. Coli

<400> 144

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agcgaagcca	gaatccccgc	gctgcgtgag	cgggccaatg	gcctgttatt	gcaagggcag	1140
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<210> 145

<211> 291

<212> DNA

<213> E. Coli

<400> 145

atgtattgcc	acgcgaaact	aaaaaatata	tcgcaacaca	cggtaatctc	cgcgcacctt	60
ttcttacctg	attattcccc	catgaatcgt	gattcctttt	atccagccat	cgctgtttt	120
ccgctgttac	tgatgctggc	cgggtgtgcg	cctatgcatg	aaaccgcga	ggcgtaaagc	180
cagcaaacgc	ccgctgcaca	agttgacacc	gcattaccca	cggcgctgaa	aatgggtggc	240
cagacagcca	atggtggctg	gagtatcacg	ataatcaact	cacttcctta	a	291

<210> 146

<211> 948

<212> DNA

<213> E. Coli

<400> 146

atgcgtgtgt	tactggcacc	gatggaggga	gtgcttgact	ctctggtgcg	tgaattgctg	60
accgaagtta	acgactacga	tctgtgcatc	accgagtttg	tccgcgtggt	ggatcaactg	120
ctgccggtaa	aagtctttca	tcgcattttg	cctgagctac	aaaacgccag	ccggacacca	180
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gccgcccgtg	cggtggagtt	aggttccttg	ggcggtggatc	tcaattgcgg	ctgcccgtcg	300
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cgtctgggct	gggacagcgg	tgagaagaaa	tttgaaatcg	ccgatgcggt	tcaacaggct	480
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cgtaaagaat	acgatgaagc	aacggaatta	tttcagcatg	ttcgggtggt	gaataattcc	900
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<210> 147
 <211> 891
 <212> DNA
 <213> E. Coli

<400> 147

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ccagacaccg	cgcgggattt	tattgatatt	catcttcccg	cgccgctgcg	caaactgtgt	120
gatttaacga	cgcttaaact	ggaaccaaac	agttttattg	atgaagacct	gcggcaatat	180
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atagagcacc	aaagtaagcc	ggaagaatta	atggcttttc	gcatgatgcg	ttattccatt	300
gcggcaatgc	aaaaccatct	tgatgcgggc	tataaagagc	ttccattggg	gctcccgatg	360
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gtgggtgccg	atgacgagat	tatgcaacac	cgcaaaatgg	cgctgttggg	gttaattcag	540
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gagaaactga	tgaccattgc	tgacagatta	cgtgaagaag	gcgcaatgca	gggcaaacac	780
gaagaagccc	tgcgtattgc	tcaggagatg	ctggatagag	gtttagacag	agagttagtt	840
atgatggtga	cccgactttc	accagacgat	cttatcgcgc	aaagccacta	a	891

<210> 148
 <211> 1668
 <212> DNA
 <213> E. Coli

<400> 148

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aatggcgcg	gtaagtcac	cctgctgcgc	attatggcgg	gcattgataa	agacatcgaa	180
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gagttcttcg	aaggtaactt	taccgagtac	gaagagtaca	agaaacgcac	gctgggcgca	1620
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<210> 149
 <211> 522
 <212> DNA
 <213> E. Coli

<400> 149
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 acatgggttg ccctctatga aaaacatgga gaaaaaggtt taattcccaa acctaaaggc 180
 gttagtgtcg atccagagtt gcgtattaag gtcgtgaaag ctgtgatcga gcagcacatg 240
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 ctgaaggtct atgaagagcg cggagaagct ggtttacgcg cgctcaagat tggcaccaaa 360
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<210> 150
 <211> 852
 <212> DNA
 <213> E. Coli

<400> 150
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 gagataccgc gcagtacgtt ttattatcat ctaaaggctc tcagcaagcc tgacaagtat 120
 gcggacgtta aaaagcgtat tagtgagatt tatcacgaga atagaggccg atacggatac 180
 cgtagggtaa cgctgtctct tcatcgagaa gggaaacaga ttaaccataa agctgttcag 240
 cgctgatgg gaaccctctc acttaaagca gcgattaagg tcaagcgata ccgctcttac 300
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 agtaataata gcgaactgaa ggatgctgtt acggaatata ttgaatacta caacagcaga 780
 agaattagcc tgaaattaaa aggtctgact ccaattgaat atcggaatca gacctatatg 840
 cctcgtgttt aa 852

<210> 151
 <211> 117
 <212> DNA
 <213> E. Coli

<400> 151
 atgaaagttc gtgcttccgt caagaaatta tgccgtaact gcaaaatcgt taagcgtgat 60
 ggtgtcatcc gtgtgatttg cagtgccgag ccgaagcata aacagcgcca aggtcga 117

<210> 152
 <211> 1332
 <212> DNA
 <213> E. Coli

<400> 152
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 cgcagactgc tgtttgttat cggcgcgctg attgtgttcc gtattggctc ttttattccg 120

atccctggta	ttgatgccgc	tgtacttgcc	aaactgcttg	agcaacagcg	aggcaccatc	180
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gggatcatgc	cgtatatctc	ggcgtcgac	attatccagc	tgctgacggg	ggttcaccca	300
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caaactctga	tgatgtccag	tcagtatgag	tctgcattga	agaaggcgaa	cctgaaaggc	1320
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<210> 153

<211> 435

<212> DNA

<213> E. Coli

<400> 153

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cgtggtatcg	gttctggcct	cggtaaaacc	gggtgctgtg	gtcacaaagg	tcagaagtct	120
cgttctggcg	gtggcgtagc	tcgcggtttc	gaggggtggc	agatgcctct	gtaccgtcgt	180
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actgttcgtg	gcctgcgtgt	tactaaaggc	gctcgtgctg	ctatcgaagc	tgctggcggt	420
aaaatcgagg	aataa					435

<210> 154

<211> 180

<212> DNA

<213> E. Coli

<400> 154

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aaggcaacgc	tgcttggcct	gggtctgcgt	cgtattggct	acaccgtaga	gcgcgaggat	120
actcctgcta	ttcgcgggat	gatcaacgcg	gtttccttca	tgggttaaagt	tgaggagtaa	180

<210> 155

<211> 504

<212> DNA

<213> E. Coli

<400> 155

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gtatctaaaa	ccgttaaagg	tggtcgtatt	ttctccttca	cagctctgac	tgtagttggc	120
gatggtaacg	gtcgcgttgg	ttttgggttac	ggtaaagcgc	gtgaagttcc	agcagcgatc	180
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ctgcaacacc	ctgttaaagg	tgttcacacg	ggttctcgcg	tattcatgca	gccggcttcc	300
gaaggtagcg	gtatcatcgc	cggtagtgca	atgcgcgccg	ttctggaagt	cgctgggggt	360
cataacgttc	tggtataaagc	ctatgggttcc	accaaccgga	tcaacgtggg	tcgtgcaact	420
attgatggcc	tggaataat	gaattctcca	gaaatggtcg	ctgccaagcg	tggtaaatcc	480
ggtgaagaaa	ttctggggaa	ataa				504

<210> 156

<211> 354

<212> DNA

<213> E. Coli

<400> 156

atggataaga	aatctgctcg	tatccgtcgt	gcgacccgcg	cacgccgcaa	gctccaggag	60
ctgggcgcaa	ctcgcttggt	ggtacatcgt	accccgcgtc	acatttacgc	acaggtaatt	120
gcaccgaacg	gttctgaagt	tctggtagct	gcttctactg	tagaaaaagc	tatcgctgaa	180
caactgaagt	acaccggtaa	caaagacgcg	gctgcagctg	tggtgaaagc	tgctcgctgaa	240
cgcgctctgg	aaaaaggcat	caaagatgta	tcctttgacc	gttccggggt	ccaatatcat	300
ggctgctgcc	aggcactggc	agatgctgcc	cgtgaagctg	gccttcagtt	ctaa	354

<210> 157

<211> 534

<212> DNA

<213> E. Coli

<400> 157

atgtctcgtg	ttgctaaagc	accggctcgtt	gttctcgccg	gcgttgacgt	aaaaatcaac	60
ggtcagggtta	ttacgatcaa	aggtaaaaaac	ggcgagctga	ctcgactct	caacgatgct	120
gttgaagtta	aacatgcaga	taataccctg	accttcggtc	cgcgtgatgg	ttacgcagac	180
ggttgggcac	aggctggtac	cgcgcgtgcc	ctgctgaact	caatggttat	cgggtgttacc	240
gaaggcttca	ctaagaagct	gcagctgggt	ggtgtaggtt	accgtgcagc	ggttaaaggc	300
aatgtgatta	acctgtctct	gggtttctct	catcctgttg	accatcagct	gcctgcgggt	360
atcactgctg	aatgtccgac	tcagactgaa	atcgtgctga	aaggcgctga	taagcagggtg	420
atcgccagc	ttgcagcgga	tctgcgcgcc	taccgtcgtc	ctgagcctta	taaaggcaag	480
ggtgttcgtt	acgccgacga	agtcgtgcgt	accaaagagg	ctaagaagaa	gtaa	534

<210> 158

<211> 393

<212> DNA

<213> E. Coli

<400> 158

atgagcatgc	aagatccgat	cgcggatatg	ctgacccgta	tccgtaacgg	tcaggccgcg	60
aacaaagctg	cggtcacat	gccttcctcc	aagctgaaag	tggaatcgc	caacgtgctg	120
aaggaagaag	gttttattga	agattttaaa	gttgaaggcg	acaccaagcc	tgaactggaa	180
cttactctga	agtattttcca	gggcaaagct	gttgtagaaa	gcattcagcg	gttcagccgc	240
ccaggctctg	gcattctataa	acgtaaagat	gagctgccga	aagttatggc	gggtctgggt	300
atcgagcttg	tttctacctc	taaagggtgtt	atgactgac	gtgcagcgcg	ccaggctgggt	360
cttggtggcg	aaattatctg	ctacgtagcc	taa			393

<210> 159

<211> 306

<212> DNA

<213> E. Coli

<400> 159

atggctaagc	aatcaatgaa	agcacgcgaa	gtaaaacgcg	tagctttagc	tgataaatac	60
ttcgcgaaac	gcgctgaact	gaaagcgatc	atctctgatg	tgaacgcttc	cgacgaagat	120

cgttggaacg	ctgtttctcaa	gctgcagact	ctgccgcgtg	attccagccc	gtctcgtcag	180
cgtaaccgct	gccgtcaaac	aggtcgtccg	catgggtttcc	tgcggaagtt	cgggttgagc	240
cgtattaagg	tccgtgaagc	cgctatgcgc	ggtgaaatcc	cgggtctgaa	aaaggctagc	300
tggtaa						306

<210> 160

<211> 540

<212> DNA

<213> E. Coli

<400> 160

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aactacaatt	ctgtcatgca	agtccctcgg	gtcgagaaga	tcaccctgaa	catgggtggt	120
ggtgaagcga	tcgctgacaa	aaaactgctg	gataacgcag	cagcagacct	ggcagcaatc	180
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tctttcgacg	gtcgtggtaa	ctacagcatg	ggtgtccgtg	agcagatcat	cttcccagaa	420
atcgactacg	ataaagtcga	ccgcgttcgt	ggtttggata	ttaccattac	caactactgcg	480
aaatctgacg	aagaaggccg	cgctctgctg	gctgcctttg	acttcccgtt	ccgcaagtaa	540

<210> 161

<211> 315

<212> DNA

<213> E. Coli

<400> 161

atggcagcga	aaatccgtcg	tgatgacgaa	gttatcgtgt	taaccggtaa	agataaagg	60
aaacgcggta	aagttaagaa	tgtcctgtct	tccggcaagg	tcattgttga	aggtatcaac	120
ctggttaaga	aacatcagaa	gccggttcgg	gccctgaacc	aaccgggtgg	catcgttgaa	180
aaagaagccg	ctattcaggt	ttccaacgta	gcaatcttca	atgcggcaac	cggcaaggct	240
gaccgtgtag	gcttttagatt	cgaagacggg	aaaaaagtcc	gtttcttcaa	gtctaacagc	300
gaaactatca	agtaa					315

<210> 162

<211> 372

<212> DNA

<213> E. Coli

<400> 162

atgatccaag	aacagactat	gctgaacgtc	gccgacaact	ccggtgcacg	tcgcgtaatg	60
tgtatcaagg	ttctgggtgg	ctcgcaccgt	cgctacgcag	gcgtaggcga	catcatcaag	120
atcaccatca	aagaagcaat	tccgcgtggg	aagggtcaaaa	aagggtgatgt	gctgaaggcg	180
gtagtggtgc	gcaccaagaa	gggtgttcgt	cgcccggcag	gttctgtcat	tcgcttcgat	240
ggtaatgctt	gtgttcttct	gaacaacaac	agcgagcagc	ctatcgggtac	gcgtattttt	300
gggccggtaa	ctcgtgagct	tcgtagttag	aagttcatga	aaattatctc	tctggcacca	360
gaagtactct	aa					372

<210> 163

<211> 567

<212> DNA

<213> E. Coli

<400> 163

atgttttaaag	gacaaaaaac	attggccgca	ctggccgtat	ctctgctggt	caactgcacct	60
gtttatgctg	ctgatgaagg	ttctggcgaa	attcacttta	agggggaggt	tattgaagca	120
ccttggtgaaa	ttcatccaga	agatattgat	aaaaacatag	atcttggaca	agtcacgaca	180

acccatataa	accgggagca	tcatagcaat	aaagtggccg	tcgacattcg	cttgatcaac	240
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tcagccgcgc	cagatcttga	cctggatgca	agctcatcag	aacagacgct	gaactttttc	480
gcctggatgg	aacaaattga	taatgcagtc	gatgtcacgg	caggtgaagt	aaccgctaac	540
gcaacctacg	tgctggatta	taaataa				567

<210> 164

<211> 1284

<212> DNA

<213> E. Coli

<400> 164

atggctgata	caaaagcaaa	actcaccctc	aacggggata	cagctgttga	actggatgtg	60
ctgaaaggca	cgctgggtca	agatgttatt	gatatccgta	ctctcggttc	aaaagggtgtg	120
ttcacctttg	accagggtt	cacttcaacc	gcatacctgcg	aatctaaaat	tactttttatt	180
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ctgttccatg	ctttccgctc	cgactcgcct	ccaatggcag	tcattgtgtg	tattaccggc	420
gcgctggcgg	cgttctatca	cgactcgcct	gatgttaaca	atcctcgtca	ccgtgaaatt	480
gccgcgttcc	gcctgctgtc	gaaaatgccg	accatggccg	cgatgtgtta	caagtattcc	540
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tggggacctg	cgcacggcgg	tgctaacgaa	gcggcgctga	aaatgctgga	agaaatcagc	840
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accgtcattt	tcgcaatggc	acgtaccgtt	ggctggatcg	cccactggag	cgaaatgcac	1200
agtgcgggta	tgaagattgc	ccgtccgcgt	cagctgtata	caggatatga	aaaacgcgac	1260
tttaaaagcg	atatcaagcg	ttaa				1284

<210> 165

<211> 1434

<212> DNA

<213> E. Coli

<400> 165

atgaaagtaa	cgctgccaga	gtttgaacgt	gcaggagtga	tgggtggttg	tgatgtgatg	60
ctggatcggt	actggtacgg	ccccaccagt	cgatatctcg	cggaagcgcc	ggtgcccggtg	120
gttaaagtga	ataccatcga	agaacgtccg	ggcggcgcg	ctaactggc	gatgaatattc	180
gcttctctcg	gtgctaattg	acgcctggtc	gggttgacgg	gcattgacga	tcgacgcgc	240
gcgctgagta	aatctctggc	cgacgtcaac	gtcaaagtcg	acttcgtttc	tgtaccgacg	300
catccgacca	ttaccaaatt	acgggtactt	tcccgcaacc	aacagctgat	ccgtctggat	360
tttgaagaag	gtttcgaagg	tggtgatccg	cagccgctgc	acgagcggtg	taatcaggcg	420
ctgagttcga	ttggcgcgct	ggtgctttct	gactacgcca	aaggtgcgct	ggcaagcgta	480
cagcagatga	tccaactggc	gcgtaaagcg	ggtgttccgg	tgctgattga	tccaaaagggt	540
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gctgttgctg	gtaaatgtaa	gaccgaagaa	gagattgttg	agcgcggcat	gaaactgatt	660
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caaccgggta	aagcgccgct	gcatatgcc	acccaagcgc	aggaaagtga	tgacgttacc	780
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gaagaagcct	gcttctttgc	caatgcggcg	gctggcgctgg	tggtcggcaa	actgggaacc	900
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ggcgcaactg	aagcggtcga	ctgggtagtg	tcgtttgaag	aggacacgcc	gcagcgcttg	1260
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gccgggagta	aagaagtctg	ggccaacggt	ggcgaagtgt	tgggtgctcaa	ctttgaagac	1380
ggttgctcga	cgaccaacat	catcaagaag	atccaacagg	ataaaaaagg	ctaa	1434

<210> 166

<211> 2841

<212> DNA

<213> E. Coli

<400> 166

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agtgcgaag	ccgggttaat	gcgcgagctg	cggtatttcc	ggcggcgcat	tatggtgcgc	300
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cgcatggggc	agcggctgat	taaagtgcgt	gatcaaccga	cgaggatggg	cttcgtctat	660
cgcggtggata	tgccgctgcg	tccgtttggc	gaaagtggcc	cgctgggtgc	gagctttgcc	720
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gatcttgacc	ttatcttcct	ccatgattgc	ccaatggatg	cgatgactga	cggtgagcgg	2160
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<210> 167
 <211> 1302
 <212> DNA
 <213> E. Coli

<400> 167						
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gaccatctca	atacgctggg	cggcgagcac	catgaccccc	tgcagttgct	gaatattttac	120
tacgaaacgc	cggataactg	gctgcgtggg	cacgatattg	gcttacgtat	tcgtggcgaa	180
aacggtcgct	atgagatgac	catgaaagtt	gcaggaagag	tgacaggcgg	cttacatcag	240
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agcaccgatt	tttatcgcg	aaaatggctg	gtggcggtcg	atggtagcca	aattgaaatc	420
gccctcgacc	agggggaagt	gaaagcgggt	gaatttgctg	aacctatctg	tgagctggaa	480
ctggaactgc	ttagcggcga	cacgcgcgcg	gtgctgaaac	tggcgaacca	actggtatcg	540
caaaccggat	tacgccaggg	cagcctgagc	aaagcggcgc	gtggctatca	tctggcgag	600
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ctgcatcacg	ctattgcgac	cgggcaacgc	atcgaaattg	aacatttccg	taatgaggca	1260
aacaatcagg	aaccgttctg	gttgcacagc	ggaaaacggt	aa		1302

<210> 168
 <211> 213
 <212> DNA
 <213> E. Coli

<400> 168						
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atcactcctg	acgatggctc	taaagatgtg	ttcgtagact	tctctgctat	ccagaacgat	120
ggttacaaat	ctctggacga	aggtcagaaa	gtgtccttca	ccatcgaaag	cggcgctaaa	180
ggcccgccag	ctggtaacgt	aaccagcctg	taa			213

<210> 169
 <211> 1572
 <212> DNA
 <213> E. Coli

<400> 169						
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cgacatatgc	cagcaggcgg	cgtctggtgg	tttaacgtcg	atcgccatga	agatgctatc	120

agtctggcga	atcaaacaat	tgcattcccag	gctgaaaccg	cacacgtcgc	ggtcattagc	180
atggacagcg	atccggcgaa	aatcttttcaa	ttagatgatt	ctcaagggcc	ggaaaaaata	240
aaattatatt	caatgctaaa	tcataaaaaa	ggctctatact	atttgaccgc	tgattttgcag	300
tggtctattg	atccccataa	ttaccttttt	attcttgttt	gcgcaataa	cgcatggcaa	360
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<210> 170

<211> 189

<212> DNA

<213> E. Coli

<400> 170

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<210> 171

<211> 1680

<212> DNA

<213> E. Coli

<400> 171

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<210> 172
 <211> 384
 <212> DNA
 <213> E. Coli

<400> 172						
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 <211> 306
 <212> DNA
 <213> E. Coli

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<210> 174
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 <212> DNA
 <213> E. Coli

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<210> 175

<211> 300
 <212> DNA
 <213> E. Coli

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 gcgatctgga cgattcgcca tcctaataatg ctggctccgt gggccagacg cggttttggc 240
 gtatggagcg cctggcgtct gggtaaaacg accctcaagc agcaacagct tcgcggttaa 300

<210> 176
 <211> 483
 <212> DNA
 <213> E. Coli

<400> 176
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 gtacgcgcga ttttaaatgcc gattctgttt attaccgctg gctggggaaa aattactggc 180
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 taa 483

<210> 177
 <211> 891
 <212> DNA
 <213> E. Coli

<400> 177
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<210> 178
 <211> 612
 <212> DNA
 <213> E. Coli

<400> 178
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<210> 179

<211> 177

<212> DNA

<213> E. Coli

<400> 179

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<210> 180

<211> 4281

<212> DNA

<213> E. Coli

<400> 180

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<210> 181

<211> 369

<212> DNA

<213> E. Coli

<400> 181

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<210> 182

<211> 711
 <212> DNA
 <213> E. Coli

<400> 182

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aagctatccc	attctgaaat	gattgaagat	aataaaaaag	acttggctgt	aaatgaccat	600
gggttgacat	gtccatcaac	aacagattgc	tcagatagat	gtagtgatta	tattaatcca	660
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<210> 183
 <211> 261
 <212> DNA
 <213> E. Coli

<400> 183

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aaacattaca	taaactatat	ggcaatacca	gaaaatgatg	gagtttttac	atggctccca	180
gatttttttc	cgcacgtagc	ggtggatata	tcaatataca	caaatgtaga	agatgattat	240
ttttttctta	tttttcctta	a				261

<210> 184
 <211> 192
 <212> DNA
 <213> E. Coli

<400> 184

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gtgtggtgta	aatatggtaa	gataccagg	caaggggatg	gtgtaaacct	tttttttggt	120
ggtgaaatta	atgttacgca	ttattttata	acaaatattg	gagctggatt	gcctgatgct	180
tgtgcagagt	aa					192

<210> 185
 <211> 504
 <212> DNA
 <213> E. Coli

<400> 185

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gcggaaatgg	acgaacagtg	gggctatgtc	ggggctaaat	cgcgccagcg	ctggctgttt	180
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tatacgacgc	gaattgagcg	gcataacctg	aatctgaggc	agcacctggc	acggctggga	420
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ctgaacataa	aacactatca	ataa				504

<210> 186
 <211> 276
 <212> DNA
 <213> E. Coli

<400> 186
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 ggcaaaagca cgcgccgaca tcagcgctat ctctgctctc actgccgtaa aacatggcaa 120
 ctgcagttca cttacaccgc ttctcaaccc ggtacgcacc agaaaatcat tgatatggcc 180
 atgaatggcg ttggatgccg ggcaacagcc cgcattatgg gcgttggcct caacacgatt 240
 ttacgtcact taaaaaactc aggccgcagt cggtaa 276

<210> 187
 <211> 417
 <212> DNA
 <213> E. Coli

<400> 187
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 aattcaacta attgcctgga gaagttatgt aatgaagtta gtattctttt taagaatcaa 180
 cctgattatc ttactttttt aagagcaatg gatggattcg aagttaatgg attacgatta 240
 tttagcctct cgattccaga accttcagtt aaaaaccttt ttgccgtaaa tgaattttat 300
 agaaataatg atgatttcat aaaccctgat ctacaagaac ggtagtgat cggggattat 360
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<210> 188
 <211> 1179
 <212> DNA
 <213> E. Coli

<400> 188
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 gaacaattat ttatgggatt tgacttctat cgaataaata gatttggtag attggaaaag 300
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 gaaaaactgg gtggagatgc aataaaaaggc tatgatcaaa tactaaatga aaaaacagcg 660
 ggcatagcga tagcaacagc atctattctt agagggtcaac aaaaacttct tgatgggtata 720
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 tatcctccca tgaaaaatat tatggaccac acaaaatga 1179

<210> 189
 <211> 666
 <212> DNA
 <213> E. Coli

<400> 189
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ggccacgccc ttgatttttg ctgcggaaaa cttagatatt ctgatgaatt aatcagtaaa 180
tttgatgaag ttacttttct agactcgaaa aggcaacttg aaagagagca aattattaga 240
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gctttcgagg atgtcgacaa aataattggg ggttacgatt tcctcctttg ctctaattgt 360
ctctctgccg ttccttgctg ggatacaatc gacaaaatag ttcttagcat caagagatta 420
ctaaaatcag gaggtgagac tcttattgta aatcaatata aaagctcata cttcaaaaaa 480
tacgaaacag gaagaaaaca tctttacgga tacattttaca aaaattcaaa aagtgtttct 540
tactatggat tactcgatga actcgcagtg caagaaatat gttcttcaca tggccttgaa 600
atattaaagt cgtggagtaa agcaggaagt tcatatgtca ctgttgggag ttgtaatgca 660
atataa 666

<210> 190
<211> 705
<212> DNA
<213> E. Coli

<400> 190
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ttaataacat taccaaccaa gtatgtccca cctattaaag atcatgagag ctttattaat 180
tgggcactat cttttggtat attaccttgt gcttttgcca tttttgcata ttttaattagc 240
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<210> 191
<211> 285
<212> DNA
<213> E. Coli

<400> 191
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ctgaccatcg ttgttgacgg taaagaaatc aaagttaaag ctcaggacgt acagcgtcac 240
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<210> 192
<211> 1977
<212> DNA
<213> E. Coli

<400> 192
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<210> 193

<211> 2634

<212> DNA

<213> E. Coli

<400> 193

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<210> 194

<211> 1572

<212> DNA

<213> E. Coli

<400> 194

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<210> 195
 <211> 1140
 <212> DNA
 <213> E. Coli

<400> 195

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<210> 196
 <211> 1371
 <212> DNA
 <213> E. Coli

<400> 196

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cagtttatcg	atggtctggc	gttgccagaa	gaagagaaag	cccgcctgaa	agcgatgacg	1320
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<210> 197

<211> 186
 <212> DNA
 <213> E. Coli

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 tctgttcacc gtgaagagat ctaccagcgt atccaggctg aaaaatccca gcagtccagt 180
 tactaa 186

<210> 198
 <211> 93
 <212> DNA
 <213> E. Coli

<400> 198
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 gcatccgggg ttcgaatccc cgcctcaccg cca 93

<210> 199
 <211> 603
 <212> DNA
 <213> E. Coli

<400> 199
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 tgttttattc atggtttccg ggcgagtga atttgtcgat tgaggatttc ggatattgat 180
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<210> 200
 <211> 597
 <212> DNA
 <213> E. Coli

<400> 200
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 gcttgcggtt atgaattggc ggagcgtggg gcagatactc gtttaattca ggattatctc 480
 gggcatcgaa atattcgcca tactgtgcgt tataccgcca gtaatgctgc tcgttttgcc 540
 ggattatggg aaagaaataa tctcataaac gaaaaattaa aaagagaaga ggtttga 597

<210> 201
 <211> 549
 <212> DNA

<213> E. Coli

<400> 201

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aacgttggtg	tgcagatcct	ggacagaacg	ggtgctgcgc	tgacgctgga	tgggtgcgaca	420
tttagttcag	aaacaacctt	gaataacgga	accaatacca	ttccgttcca	ggcgcgttat	480
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<210> 202

<211> 648

<212> DNA

<213> E. Coli

<400> 202

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agattatttc	tattagcgtc	gttgctgcca	atgtttgctc	tggccggaaa	taaatggaat	180
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gatgtgcttt	ccgtgggaga	ggggccaggg	atagccacca	atattggcgt	agcgttggtt	480
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tcaggctcta	cttcgctaca	tttcatcgcc	aaatatcggtg	ctaccggggc	tcgggttact	600
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<210> 203

<211> 726

<212> DNA

<213> E. Coli

<400> 203

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gcattgggtg	ctccaatggg	cgaaagcacg	gttaaaattgc	cttctgatgc	aggaagcaat	660
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<210> 204

<211> 2637

<212> DNA

<213> E. Coli

<400> 204

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cctttgtcat	ctgccgacct	ctattttta	ccgcgctttt	tagcggatga	tccccaggct	180
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<210> 205

<211> 531

<212> DNA

<213> E. Coli

<400> 205

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ccgggtaaac	caaatacgcg	gaattttttac	gcccggctaa	tggcgacaca	ggtgcctgtc	480
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<210> 206

<211> 504

<212> DNA

<213> E. Coli

<400> 206

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<210> 207

<211> 903

<212> DNA

<213> E. Coli

<400> 207

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<210> 208

<211> 1631

<212> DNA

<213> E. Coli

<400> 208

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<210> 209

<211> 534

<212> DNA

<213> E. Coli

<400> 209

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gcataccgcg	atggttctgg	catatggacc	atctgtcggg	gtgccacagt	ggtggatgga	180
aaaaccggtt	ttcccaatat	gaaactgtcg	aaggaaaaat	gcgaccaggt	caacgccatt	240
gagcgtgata	aggcgctggc	atgggtggag	cgcaatatta	aagtaccact	gaccgaacca	300
caaaaagcgg	gtatcgcgct	attttgtccc	tataacattg	gccccggtaa	gtgtttcccg	360
tcgacgtttt	ataagcggtc	gaatgctggg	gatcgtaaag	gtgcatgcga	agcgattcgc	420
tgggtggatta	aggatggcgg	acgcgattgc	cgcatctcgt	caaataactg	ttacggtcag	480
gttattcgtc	gtgaccagga	gagcgcatta	acctgctggg	ggatagaaca	gtga	534

<210> 210

<211> 312

<212> DNA

<213> E. Coli

<400> 210

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gtaactgtag	ccttacagga	caaagaacgc	tttgacggtg	aaatttttga	cctggatgtc	120
gccatggacc	gtgttgaaag	agctgcgctg	gagttttatg	aggcagcagc	cagaaggagc	180
gtccggcaag	tcttcctgga	agtagcagaa	aaattgtcag	aaaaagttga	gtcttatctg	240
cagcatcagt	actcctttta	gattgaaaat	cctgccaaata	agcacgagcg	tcctcatcat	300
aaatatctat	ga					312

<210> 211

<211> 291

<212> DNA

<213> E. Coli

<400> 211

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catcggggtg	aggatatgaa	atcaatggat	aagttaacaa	caggtgttgc	ctatggcaca	120
tggcggggta	atgctggttt	ctgggcattg	cagttactcg	ataaagtaac	tccgtcacag	180
tgggctgcaa	tcggtgtgct	gggtagcctg	gtttttggcc	tgctgacgta	tctgacaaat	240
ctttatttca	agattaaaga	agacaggcgt	aaggctgcga	gaggagagta	a	291

<210> 212

<211> 216

<212> DNA

<213> E. Coli

<400> 212

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atcttctcctg	ttgatggtag	taaagatgtg	tttgtgcatt	tttctgcgat	tcagaatgat	120
aattatcgaa	ccttatttga	aggtcaaaaag	gttaccttct	ctatagagag	tggtgctaaa	180
ggtcctgcag	cagcaaatgt	catcattact	gattaa			216

<210> 213

<211> 1017

<212> DNA

<213> E. Coli

<400> 213

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gagcagattc	tgccatggca	aaacatgggtg	gaagtcacg	agccgtttta	ccccaaggct	180
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cgccacctgc	tggagcagca	tcaactggcc	cgccaattgt	tcaagaccat	caatcgctgg	420
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gcaccagct	cgaccaagaa	caaagagcag	caacgcgatc	cggagatgca	tcagaccaag	540
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agaaccttga	aacagcatcc	acgcaagaac	aaaacggcca	tcaacatcga	atacatgaaa	840
gccagcatcc	gggccagggt	ggagcaccca	tttcgcatca	tcaagcgaca	gttcggcttc	900
gtgaaagcca	gatacaaggg	gttgctgaaa	aacgataaacc	aactggcgat	gttattcacg	960
ctggccaacc	tgtttcgggc	ggaccaaatg	atacgtcagt	gggagagatc	tcactaa	1017

<210> 214

<211> 474

<212> DNA

<213> E. Coli

<400> 214

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ttattgaaac	aaatatgcca	gcattatgca	ggcctggact	atattagtg	aggtgtatac	180
ggctttggtc	ataataataa	tattgcgggtg	gcgtatgtaa	aggaaaaata	tagaccgca	240
gatgatgatt	acattttgtt	tttgaatccc	gatatcatca	tgaagcatga	tgatttgctg	300
acatatatta	aatatgtcga	aagtaagcgt	tatgctttta	gtacattatg	cctgttccga	360
gatgaagcga	aatctttaca	tgattattcc	gtaagaaaat	ttcctgtgct	ttctgatttt	420
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<210> 215

<211> 1119
 <212> DNA
 <213> E. Coli

<400> 215

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gtccattctg	ctaaagagtt	aaaagaaagt	tatccatggg	ttaaattcat	tgagtttcct	180
gaggttaaag	ggtcgtggct	aaaacgtttg	cactttgaat	atgtagtttg	taaaaaactt	240
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actaaaaaaa	gatatgtgta	ttgtcataac	cctgcacctt	tttataaagg	aattttattc	360
cgtgaaattc	ttatggagcc	tagctttttc	ttatttaaaa	tgctatacgg	gctgatatat	420
aaaataaaca	ttaaaaaaa	tactgcagtg	tttgttcaac	aattctggat	gaaagaaaaa	480
tttatcaaga	aatattctat	aaataacatc	attgtcagtc	ggccagaaat	taaattatct	540
gataaaagcc	aacttactga	tgatgattct	caatttaaga	ataacccttc	tgagttgaca	600
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tttgattcta	ataacgatga	catgttagtt	aaacttatta	ttgacttcaa	aaaaggtaac	1020
ctcaaaaaag	atatctctga	tgcaaatctt	atttatcgta	atgaaaatgt	attagttggg	1080
tttgatgaac	tagttaattt	tattactgaa	gaacattga			1119

<210> 216
 <211> 591
 <212> DNA
 <213> E. Coli

<400> 216

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cgcaatgatg	gtagcattaa	ttttggtgaa	aatttcacaa	gtggagtcgg	tctcaggctg	180
gatgcatttg	gacgtggcgt	gatttttttt	tccgataatg	tgcaagttaa	cgactatggt	240
catatcgctt	caattgagag	cgttacgata	ggtcgggata	cgcttattgc	aagtaaagta	300
tttattaccg	atcataatca	cggttccttt	aagcactctg	atccaatgag	ttcgccaaat	360
atacctccag	acatgcgcac	gttggaatct	tcagctgttg	taattggcca	gagggtttgg	420
ttgggtgaga	atgtgacggt	tttgcttgga	acaattattg	gtaatggagt	cgtagtcggc	480
gccaaattctg	ttgttagagg	ttctattccc	gaaaatactg	tcattgcggg	agtaccagca	540
aaaatcataa	agaaatacaa	tcatgagacc	aaattatggg	aaaaagcata	g	591

<210> 217
 <211> 993
 <212> DNA
 <213> E. Coli

<400> 217

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gatgcactgg	acattgcttc	agattatgaa	aacatttctg	ttgttaacat	tcctctatgg	120
ggtggagtag	tccagagaat	tattagttct	gttaagctta	gtacatttct	ctgcggtcct	180
gaaaataaag	atgttttaat	tttcaatttc	ccgatggcca	aaccattttg	gcatatattg	240
tcattctttc	accgccttct	aaaatttaga	atagtacctc	tgattcatga	tattgatgaa	300
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ataaaaaat	ttgattacct	cgtctcatct	gatgtggagc	atcgagatgt	tacggataag	480
caacgagggg	tcatatatgc	tggcaacctt	tctaggcata	aatgttcttt	catatatact	540

gaaggatgcg	atcttactct	ctttggtgtc	aactatgaaa	ataaagataa	tcctaaatat	600
cttggaagtt	ttgatgctca	atctccggaa	aagattaacc	tcccaggcat	gcaatttgga	660
ctcatttgga	atggagattc	tgtcgaaacc	tgtagtgggtg	cctttggcga	ctattttaaag	720
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gataaagccg	cccttgcgga	tttcattgta	gataatagaa	taggatatgc	agtgggatca	840
atcaaagaaa	tgcaagagat	tgttgactcc	atgacaatag	aaacttataa	gcaaattagt	900
gagaatacaa	aaattatttc	tcagaaaatt	cgaacaggaa	gttacttcag	ggatgttctt	960
gaagaggtga	tcgatgatct	taaaactcgc	taa			993

<210> 218

<211> 1167

<212> DNA

<213> E. Coli

<400> 218

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tatgaaataa	cgtcagatat	atatgctttt	cagttaaatg	acgctacgtt	gatttttcta	180
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ggcttgtag	ttatttcttt	ttcgatgata	tatatatgca	tgaggttaag	taactaccag	360
ttcgggacta	gcttacttag	ctatatgaat	ttgataagag	atgctgatgt	tgaagacaca	420
tcaagaaatt	tctcagcata	catgcagcca	atcattctaa	ctacttttgc	tttattttatt	480
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gtattcatct	ttgcaattat	actgaatact	ggtaagcaaa	ttgtctttat	ggttatcatc	600
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ttcatgacta	atattagcag	ttggatacaa	ataactcttt	gtatcatagt	attctctcaa	1140
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<210> 219

<211> 1104

<212> DNA

<213> E. Coli

<400> 219

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aaaaagctaa	acaaaaaagt	tttagtgatt	gagaaaaagaa	atcatatcgg	tggaaatgcg	120
tacacagagg	actgtgaggg	tatccagatt	cataaatatg	gtgcacatat	ttttcatacc	180
aatgataaat	atatatggga	ttacgttaat	gatttagtag	aatttaatcg	ttttactaat	240
tctccactgg	cgattttataa	agacaaatta	ttcaaccttc	cttttaatat	gaatactttc	300
caccaaagt	ggggagttaa	agatcctcaa	gaagctcaaa	atatcattaa	tgctcagaaa	360
aaaaagtatg	gtgacaaggt	acctgaaaat	ttggaggagc	aggcgatttc	attagttggg	420
gaggacttat	accaagcatt	gataaagggt	tatacggaga	agcagtgggg	aagaagtgca	480
aaagaattgc	ctgcatttat	tattaagcga	atcccagtga	gatttacgtt	tgataacaat	540
tatttttccg	atcgctatca	aggtattccg	gtgggaggct	acactaagct	tattgaaaaa	600
atgcttgaag	gtgtggacgt	aaaattaggc	attgatTTTT	tgaaagacaa	agattctcta	660
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ttccaaggga	atgcagtaat	aaatttcact	gatgctaatt	taccatatac	cagaataatt	840
gagcataaac	attttgacta	tgttgagaca	aagcatacgg	ttgttacaaa	agaatatcca	900

ttagagtgga	aagttggcga	cgaaccctac	tatccagtta	atgataataa	aaacatggag	960
ctttttaaga	aatatagaga	gttagctagc	agagaagaca	aggttatatt	tggcgggct	1020
ttggccgagt	ataaatatta	tgatatgcat	caagtgatat	ctgccgctct	ttatcaagt	1080
aaaaatataa	tgagtacgga	ttaa				1104

<210> 220

<211> 1116

<212> DNA

<213> E. Coli

<400> 220

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gtcagactac	cccggtgcgtt	tggcctggct	ggcatgttct	taccgattgc	ttcaacgctg	180
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<210> 221

<211> 1404

<212> DNA

<213> E. Coli

<400> 221

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gcctataccg	atgctaacta	cctcgggtggt	ggtgacgtag	atcaagactg	gtccgcgaac	1380
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<210> 222
 <211> 669
 <212> DNA
 <213> E. Coli

<400> 222						
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attgaacaaa	atcaactctg	gcgagacgct	ttttactggt	tagcctggca	aaatagaatt	420
ctggaattac	gcgacgtgca	gctcattggg	cataattcct	acgaacaaat	ccgcgcaaca	480
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<210> 223
 <211> 255
 <212> DNA
 <213> E. Coli

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acgaccaaac	tgacgtaca	tgacgagaac	aacgaatgcg	gtatcgggtga	cgtggttgaa	180
atccgcgaat	gccgtccgct	gtccaagact	aaatcctgga	cgctggttcg	cgttgtagag	240
aaagcggttc	tgtaa					255

<210> 224
 <211> 192
 <212> DNA
 <213> E. Coli

<400> 224						
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cacctgttga	agcaagtgcg	tcgcgatgtc	gcacgcgtta	agactttact	gaacgagaag	180
gcgggtgcgt	aa					192

<210> 225
 <211> 411
 <212> DNA
 <213> E. Coli

<400> 225						
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gcgcagggtta	cggatgttag	cttcggcagc	ttcggctctga	aagctgttgg	ccgtggctcg	120
ctgactgccc	gtcagatcga	agcagcacgt	cgtgctatga	cccgtgcagt	taagcgtcaa	180
ggtaagatct	ggatccgtgt	gttcccggac	aaaccgatca	ctgaaaagcc	gctggcagtg	240

cgtatgggta	aaggtaaagg	taacgtggag	tattgggttg	ccttgattca	gccgggtaaa	300
gtcctgtatg	aaatggacgg	tgttccggaa	gagctggccc	gtgaagcatt	caagctggca	360
gcagcgaaac	tgccgattaa	aaccaccttt	gtaactaaga	cggatgatga	a	411

<210> 226
 <211> 702
 <212> DNA
 <213> E. Coli

<400> 226						
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cagtacctga	ctaaggaact	ggctaaagcg	tccgtatctc	gtatcgttat	cgagcgctcg	180
gctaagagca	tccgtgtaac	cattcacact	gctcgcccg	gtatcgttat	cggtaaaaaa	240
ggtgaagacg	tagaaaaact	gcgtaaggtc	gtagcggaca	tcgctggcgt	tcctgcacag	300
atcaacatcg	ccgaagttcg	taagcctgaa	ctggacgcaa	aactggttgc	tgacagcatc	360
acttctcagc	tggaacgtcg	cgttatgttc	cgctcgtgcta	tgaagcgtgc	tgtacagaac	420
gcaatgcgtc	tgggcgctaa	aggtattaaa	gttgaagtta	gcggccgtct	gggcggcgcg	480
gaaatcgcac	gtaccgaatg	gtaccgcgaa	ggtcgcgtac	cgctgcacac	tctgcgtgct	540
gacatcgact	acaacacctc	tgaagcgcac	accacttacg	gtgtaatcgg	cgttaaagtg	600
tggatcttca	aaggcgagat	cctgggtggg	atggctgctg	ttgaacaacc	ggaaaaaccg	660
gctgctcagc	ctaaaaagca	gcagcgtaaa	ggccgtaaat	aa		702

<210> 227
 <211> 333
 <212> DNA
 <213> E. Coli

<400> 227						
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aagaaagcgg	ctgtactggt	caagaaagtt	ctggaatctg	ccattgctaa	cgctgaacac	180
aacgatggcg	ctgacattga	cgatctgaaa	gttacgaaaa	ttttcgtaga	cgaaggcccc	240
agcatgaagc	gcattatgcc	gcgtgcaaaa	ggctcgtgcag	atcgcatcct	gaagcgcacc	300
agccacatca	ctgtgggtgt	gtccgatcgc	tga			333

<210> 228
 <211> 279
 <212> DNA
 <213> E. Coli

<400> 228						
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aaagcggtgg	aaagcggaga	caagaagccc	ctgcgcactt	ggccccgtcg	ttcaacgatc	120
tttcttaaca	tgatcggttt	gaccatcgct	gtccataatg	gtcgtcagca	cgttccggta	180
tttgaaccg	acgaaatggt	tggtcacaaa	ctgggtgaat	tcgcaccgac	tcgtacttat	240
cgcggccacg	ctgctgataa	aaaagcgaag	aagaaataa			279

<210> 229
 <211> 822
 <212> DNA
 <213> E. Coli

<400> 229						
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aaccctgagc	tgcaacaagg	caaacctttt	gctccgttgc	tggaaaaaaa	cagcaaatcc	120
ggtggtcgtg	acaacaatgg	ccgtatcacc	actcgtcata	tcggtggtgg	ccacaagcag	180

gcttaccgta	ttgttgactt	caaacgcaac	aaagacggta	tcccggcagt	tgttgaacgt	240
cttgagtacg	atccgaaccg	ttccgcgaac	atcgcgctgg	ttctgtacaa	agacggtgaa	300
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atgctgcgcg	ttctgggtaa	agcaggtgct	gcacgctggc	gtgggtgttcg	tccgaccgtt	660
cgcggtaccg	cgatgaaccc	ggtagaccac	ccacatgggtg	gtgggtgaagg	tcgtaacttt	720
ggtaagcacc	cggttaactcc	gtggggcggt	cagaccaaag	gtaagaagac	ccgcagcaac	780
aagcgtactg	ataaattcat	cgtacgtcgc	cgtagcaa	aa		822

<210> 230

<211> 303

<212> DNA

<213> E. Coli

<400> 230

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gcagaaatca	aagctgctgt	gcagaaactg	tttgaagtcg	aagtcgaagt	cgttaacacc	180
ctggtagtta	aagggaaggt	taaacgtcac	ggacagcgta	tcggtcgtcg	tagcgactgg	240
aaaaaagctt	acgtcacctt	gaaagaaggc	cagaatctgg	acttcgttgg	cggcgctgag	300
taa						303

<210> 231

<211> 630

<212> DNA

<213> E. Coli

<400> 231

atgattgggt	tagtcggtaa	aaaagtgggt	atgaccgta	tcttcacaga	agacggcggt	60
tctatcccag	taaccgtaat	cgaagttgaa	gcaaaccg	ttactcaggt	taaagacctg	120
gctaacgatg	gctaccgtgc	tattcaggtg	accaccgggtg	ctaaaaaagc	taaccgtgtg	180
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gaattccgcc	tggctgaagg	cgaagagttc	actgtaggtc	agagcattag	cgttgaactg	300
tttgctgacg	ttaaaaaagt	tgacgtaact	ggcacctcta	aaggtaaagg	tttcgcaggt	360
accgttaagc	gctggaactt	ccgtaccag	gacgctactc	acggtaaactc	cttgtctcac	420
cgcgttccgg	gttctatcgg	tcagaaccag	actccgggca	aagtgttcaa	aggcaagaaa	480
atggcaggtc	agatgggtaa	cgaacgtgta	accgttcaga	gccttgacgt	agtacgcgtt	540
gacgtgagc	gcaacctgct	gctgggttaa	ggtgctgtcc	cgggtgcaac	cggtagcgac	600
ctgatcggtta	aaccagctgt	gaaggcgtaa				630

<210> 232

<211> 606

<212> DNA

<213> E. Coli

<400> 232

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cagggctactc	gtgctcagaa	gactcgtgct	gaagtaactg	gttccggtaa	aaaaccgtgg	180
cgccagaaaag	gcaccggccg	tgcgcgttct	ggttctatca	agagcccgat	ctggcggttct	240
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taccgcggcg	cgctgaaaag	catcctgtcc	gaactgggtac	gtcaggatcg	tctgatcggt	360
gtcgagaagt	tctctgtaga	agcgccgaaa	actaagctgc	tggcacagaa	actgaaagac	420
atggctctgg	aagatgtgct	gatcatcacc	ggtgagctgg	acgaaaacct	gttcctggct	480

gcgcgcaacc	tgacacaaggt	tgacgtacgc	gatgcaactg	gtatcgaccc	ggttagcctg	540
atcgcccttcg	acaaagtcgt	aatgactgct	gatgctgtta	agcaagttga	ggagatgctg	600
gcatga						606

<210> 233
 <211> 312
 <212> DNA
 <213> E. Coli

<400> 233						
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gcaaccgcgg	aaatcgtcga	gactgccaaag	cgcactgggtg	cgcaggtccg	tggtccgatac	120
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gcgcgcgatac	agtacgaaat	ccgtactcac	ttgcgtctgg	ttgacatcgt	tgagccaacc	240
gagaaaaccg	ttgatgctct	gatgcgtctg	gatctggctg	ccggtgtaga	cgtgcagatac	300
agcctgggtt	aa					312

<210> 234
 <211> 357
 <212> DNA
 <213> E. Coli

<400> 234						
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gctaaaggct	actacgggtc	gcgttctcgc	gtataccgcg	ttgccttcca	ggctgttatc	120
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<210> 235
 <211> 198
 <212> DNA
 <213> E. Coli

<400> 235						
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ggttttaagc	acaagcacgc	taacctgcgt	cacattctga	ccaaaaaagc	gaccaaaccgt	120
aaacgtcacc	tgcgctccga	agccatgggt	tccaaaggcg	atctgggcct	ggtaatcgcg	180
tgctgcccgt	acgcataa					198

<210> 236
 <211> 543
 <212> DNA
 <213> E. Coli

<400> 236						
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gccaggaag	ttcgcttaac	aggtctggaa	ggcgagcagc	ttggtattgt	gagtctgaga	120
gaagctctgg	agaaagcaga	agaagccgga	gtagacttag	tcgagatcag	ccctaaccgcc	180
gagccgccgg	ttgtcgtat	aatggattac	ggcaaattcc	tctatgaaaa	gagcaagtct	240
tctaaggaac	agaagaaaaa	gcaaaaagt	atccagggtta	aggaaattaa	attccgtcct	300
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ggtatggaag	tgcttaatcg	cgtgaaagac	gatttgcaag	aactggcagt	ggtcgaatcc	480
ttcccaacga	agatcgaagg	ccgccagatg	atcatgggtgc	tcgctcctaa	gaagaaacag	540
taa						543

<210> 237
 <211> 1929
 <212> DNA
 <213> E. Coli

<400> 237

atgcctgtta	taactcttcc	tgatggcagc	caacgccatt	acgatcacgc	tgtaagcccc	60
atggatgttg	cgctggacat	tggtccaggt	ctggcgaaaag	cctgtatcgc	agggcgcggtt	120
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gagaagcgga	tgcattgagct	tgctgagaaa	aactacgacg	tcattaagaa	gaaagtcagc	420
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<210> 238
 <211> 1353
 <212> DNA
 <213> E. Coli

<400> 238

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<210> 239

<211> 2904

<212> DNA

<213> E. Coli

<400> 239

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ctctaccccc	ggagatgaat	tcacgaggcg	ctacctaaat	agctttcggg	gagaaccagc	2100
tatctcccg	tttgattggc	ctttcacccc	cagccacaag	tcacccgcta	atttttcaac	2160
attagtcggt	tcggtcctcc	agtttagtgtt	acccaacctt	caacctgccc	atggctagat	2220

caccggggtt	cggggtctata	ccctgcaact	taacgcccag	ttaagactcg	gtttcccttc	2280
ggctccccta	ttcggttaac	cttgctacag	aatataagtc	gctgacccat	tatacaaaag	2340
gtacgcagtc	acacgcctaa	gcggtgctccc	actgcttgta	cgtacacggg	ttcaggttct	2400
ttttcactcc	cctcgccggg	gttctttttcg	cctttccctc	acggtagctg	ttcactatcg	2460
gtcagtcagg	agtatttagc	cttgaggat	ggcccccca	tattcagaca	ggataccacg	2520
tgtcccgcgc	tactcatcga	gctcacagca	tgtgcatttt	tgtgtacggg	gctgtcaccc	2580
tgtatcgcg	gcctttccag	acgcttccac	taacacacac	actgattcag	gctctgggct	2640
gctccccgtt	cgctcgccgc	tactggggga	atctcggttg	atttcttttc	ctcggggtac	2700
ttagatgttt	cagttccccc	ggttcgccct	attaacctat	ggattcagtt	aatgatagt	2760
tgtcgaaaca	cactgggttt	ccccattcgg	aaatcgccgg	ttataacggg	tcatatcacc	2820
ttaccgacgc	ttatcgcgaga	ttagcacgtc	cttcatcgcc	tctgactgcc	agggcatcca	2880
ccgtgtacgc	ttagtcgctt	aacc				2904

<210> 240
 <211> 120
 <212> DNA
 <213> E. Coli

<400> 240						
atgcctggca	gttccctact	ctcgcatggg	gagaccccac	actaccatcg	gcgctacggc	60
gtttcacttc	tgagttcggc	atggggtcag	gtgggaccac	cgcgctacgg	ccgccaggca	120

<210> 241
 <211> 76
 <212> DNA
 <213> E. Coli

<400> 241						
gtcccccttcg	tctagaggcc	caggacaccg	ccctttcacg	gcggtaacag	gggttcgaat	60
cccctagggg	acgcca					76

<210> 242
 <211> 1549
 <212> DNA
 <213> E. Coli

<400> 242						
aaattgaaga	gtttgatcat	ggctcagatt	gaacgctggc	ggcaggccta	acacatgcaa	60
gtcgaacggg	aacaggaagc	agcttgctgc	ttcgctgacg	agtggcggac	gggtgagtaa	120
tgtctgggaa	gctgcctgat	ggagggggat	aactactgga	aacggtagct	aataccgcat	180
aatgtcgcaa	gaccaaagag	ggggaccttc	gggcctcttg	ccatcggatg	tgcccagatg	240
ggattagctt	gttgggtggg	taacgggtca	ccaaggcgac	gatccctagc	tggctctgaga	300
ggatgaccag	ccacactgga	actgagacac	gtccagact	cctacgggag	gcagcagtgg	360
ggaatattgc	acaatgggag	caagcctgat	gcagccatgc	cgcgtgtatg	aagaaggcct	420
tcgggttgta	aagtactttc	agcggggagg	aagggaagtaa	agttaatacc	tttgctcatt	480
gacgttacct	gcagaagaag	caccgggctaa	ctccgtgcc	gcagccgcgg	taatacggag	540
gggtcaagcg	ttaatcgga	ttactgggag	taaagcgcac	gcaggcgggt	tggttaaagtc	600
agatgtgaaa	tccccgggct	caacctggga	actgcatctg	atactggcaa	gcttgagtct	660
cgtagagggg	ggtagaattc	caggtgtagc	ggtgaaatgc	gtagagatct	ggaggaatac	720
cggtggcgaa	ggcgccccc	tggacgaaga	ctgacgctca	gggtgcgaaag	cgtggggagc	780
aaacaggatt	agataccctg	gtagtccacg	ccgtaaacga	tgtcgacttg	gaggttggtc	840
ccttgaggcg	tggcttccgg	agctaacgcg	ttaagtcgac	cgctggggga	gtacggccgc	900
aagggttaaaa	ctcaaatgaa	ttgacggggg	cccgcacaag	cggtggagca	tgtggtttaa	960
ttcgatgcaa	cgcgaagaac	cttacctggt	cttgacatcc	acggaagtgt	tcagagatga	1020
gaatgtgcct	tcgggaaccg	tgagacaggt	gctgcatggc	tgtcgtcagc	tcgtgtgtgt	1080
aaatgttggg	ttaaagtccc	caacgagcgc	aacccttata	ctttgttgcc	agcgggtccgg	1140
ccgggaactc	aaaggagact	gccagtgata	aactggagga	aggtggggat	gacgtcaagt	1200

catcatggcc	cttacgacca	gggctacaca	cgtgctacaa	tggcgcatac	aaagagaagc	1260
gacctcgcgga	gagcaagcgg	acctcataaa	gtgcgtcgta	gtccggattg	gagtctgcaa	1320
ctcgactcca	tgaagtcgga	atcgctagta	atcgtggatc	agaatgccac	ggtgaatacg	1380
ttcccggggcc	ttgtacacac	cgcccgtcac	accatgggag	tggggttgcaa	aagaagtagg	1440
tagcttaacc	ttcggggagg	cgcttaccac	tttgtgattc	atgactgggg	tgaagtcgta	1500
acaaggtaac	cgtaggggaa	cctgcgggtt	gatcacctcc	ttaccttaa		1549

<210> 243

<211> 221

<212> PRT

<213> E. Coli

<400> 243

Met	Asn	Val	Phe	Ser	Gln	Thr	Gln	Arg	Tyr	Lys	Ala	Leu	Phe	Trp	Leu
1				5					10					15	
Ser	Leu	Phe	His	Leu	Leu	Val	Ile	Thr	Ser	Ser	Asn	Tyr	Leu	Val	Gln
			20					25					30		
Leu	Pro	Val	Ser	Ile	Leu	Gly	Phe	His	Thr	Thr	Trp	Gly	Ala	Phe	Ser
		35					40					45			
Phe	Pro	Phe	Ile	Phe	Leu	Ala	Thr	Asp	Leu	Thr	Val	Arg	Ile	Phe	Gly
	50				55					60					
Ala	Pro	Leu	Ala	Arg	Arg	Ile	Ile	Phe	Ala	Val	Met	Ile	Pro	Ala	Leu
65				70						75					80
Leu	Ile	Ser	Tyr	Val	Ile	Ser	Ser	Leu	Phe	Tyr	Met	Gly	Ser	Trp	Gln
			85					90					95		
Gly	Phe	Gly	Ala	Leu	Ala	His	Phe	Asn	Leu	Phe	Val	Ala	Arg	Ile	Ala
			100					105					110		
Thr	Ala	Ser	Phe	Met	Ala	Tyr	Ala	Leu	Gly	Gln	Ile	Leu	Asp	Val	His
	115						120					125			
Val	Phe	Asn	Arg	Leu	Arg	Gln	Ser	Arg	Arg	Trp	Trp	Leu	Ala	Pro	Thr
	130					135					140				
Ala	Ser	Thr	Leu	Phe	Gly	Asn	Val	Ser	Asp	Thr	Leu	Ala	Phe	Phe	Phe
145					150				155						160
Ile	Ala	Phe	Trp	Arg	Ser	Pro	Asp	Ala	Phe	Met	Ala	Glu	His	Trp	Met
			165					170						175	
Glu	Ile	Ala	Leu	Val	Asp	Tyr	Cys	Phe	Lys	Val	Leu	Ile	Ser	Ile	Val
	180							185					190		
Phe	Phe	Leu	Pro	Met	Tyr	Gly	Val	Leu	Leu	Asn	Met	Leu	Leu	Lys	Arg
	195					200					205				
Leu	Ala	Asp	Lys	Ser	Glu	Ile	Asn	Ala	Leu	Gln	Ala	Ser			
	210					215					220				

<210> 244

<211> 203

<212> PRT

<213> E. Coli

<400> 244

Met	Ile	Arg	Trp	Met	Asn	Glu	Pro	Leu	Trp	Pro	Phe	Ile	Glu	Arg	Lys
1				5					10					15	
Lys	Ser	Met	Arg	Asn	Leu	Val	Lys	Tyr	Val	Gly	Ile	Gly	Leu	Leu	Val
		20						25					30		
Met	Gly	Leu	Ala	Ala	Cys	Asp	Asp	Lys	Asp	Thr	Asn	Ala	Thr	Ala	Gln
	35					40					45				
Gly	Ser	Val	Ala	Glu	Ser	Asn	Ala	Thr	Gly	Asn	Pro	Val	Asn	Leu	Leu

50		55		60
Asp Gly Lys Leu Ser Phe Ser Leu Pro Ala Asp Met Thr Asp Gln Ser				
65		70		75
Gly Lys Leu Gly Thr Gln Ala Asn Asn Met His Val Trp Ser Asp Ala				80
	85		90	95
Thr Gly Gln Lys Ala Val Ile Val Ile Met Gly Asp Asp Pro Lys Glu				
	100		105	110
Asp Leu Ala Val Leu Ala Lys Arg Leu Glu Asp Gln Gln Arg Ser Arg				
	115		120	125
Asp Pro Gln Leu Gln Val Val Thr Asn Lys Ala Ile Glu Leu Lys Gly				
	130		135	140
His Lys Met Gln Gln Leu Asp Ser Ile Ile Ser Ala Lys Gly Gln Thr				
145		150		155
Ala Tyr Ser Ser Val Ile Leu Gly Asn Val Gly Asn Gln Leu Leu Thr				160
	165		170	175
Met Gln Ile Thr Leu Pro Ala Asp Asp Gln Gln Lys Ala Gln Thr Thr				
	180		185	190
Ala Glu Asn Ile Ile Asn Thr Leu Val Ile Gln				
	195		200	

<210> 245
 <211> 324
 <212> PRT
 <213> E. Coli

<400> 245

Met Ala Asn Met Phe Ala Leu Ile Leu Val Ile Ala Thr Leu Val Thr				
1		5		10
Gly Ile Leu Trp Cys Val Asp Lys Phe Phe Phe Ala Pro Lys Arg Arg				15
	20		25	30
Glu Arg Gln Ala Ala Ala Gln Ala Ala Ala Gly Asp Ser Leu Asp Lys				
	35		40	45
Ala Thr Leu Lys Lys Val Ala Pro Lys Pro Gly Trp Leu Glu Thr Gly				
	50		55	60
Ala Ser Val Phe Pro Val Leu Ala Ile Val Leu Ile Val Arg Ser Phe				
65		70		75
Ile Tyr Glu Pro Phe Gln Ile Pro Ser Gly Ser Met Met Pro Thr Leu				80
	85		90	95
Leu Ile Gly Asp Phe Ile Leu Val Glu Lys Phe Ala Tyr Gly Ile Lys				
	100		105	110
Asp Pro Ile Tyr Gln Lys Thr Leu Ile Glu Thr Gly His Pro Lys Arg				
	115		120	125
Gly Asp Ile Val Val Phe Lys Tyr Pro Glu Asp Pro Lys Leu Asp Tyr				
	130		135	140
Ile Lys Arg Ala Val Gly Leu Pro Gly Asp Lys Val Thr Tyr Asp Pro				
145		150		155
Val Ser Lys Glu Leu Thr Ile Gln Pro Gly Cys Ser Ser Gly Gln Ala				
	165		170	175
Cys Glu Asn Ala Leu Pro Val Thr Tyr Ser Asn Val Glu Pro Ser Asp				
	180		185	190
Phe Val Gln Thr Phe Ser Arg Arg Asn Gly Gly Glu Ala Thr Ser Gly				
	195		200	205
Phe Phe Glu Val Pro Lys Asn Glu Thr Lys Glu Asn Gly Ile Arg Leu				
	210		215	220
Ser Glu Arg Lys Glu Thr Leu Gly Asp Val Thr His Arg Ile Leu Thr				
225		230		235
				240

Val	Pro	Ile	Ala	Gln	Asp	Gln	Val	Gly	Met	Tyr	Tyr	Gln	Gln	Pro	Gly
				245					250					255	
Gln	Gln	Leu	Ala	Thr	Trp	Ile	Val	Pro	Pro	Gly	Gln	Tyr	Phe	Met	Met
			260					265					270		
Gly	Asp	Asn	Arg	Asp	Asn	Ser	Ala	Asp	Ser	Arg	Tyr	Trp	Gly	Phe	Val
		275					280					285			
Pro	Glu	Ala	Asn	Leu	Val	Gly	Arg	Ala	Thr	Ala	Ile	Trp	Met	Ser	Phe
	290					295					300				
Asp	Lys	Gln	Glu	Gly	Glu	Trp	Pro	Thr	Gly	Leu	Arg	Leu	Ser	Arg	Ile
305					310					315					320
Gly	Gly	Ile	His												

<210> 246
 <211> 586
 <212> PRT
 <213> E. Coli

<400> 246

Met	Thr	Ile	Thr	Lys	Leu	Ala	Trp	Arg	Asp	Leu	Val	Pro	Asp	Thr	Asp
1				5					10					15	
Ser	Tyr	Gln	Glu	Ile	Phe	Ala	Gln	Pro	His	Leu	Ile	Asp	Glu	Asn	Asp
			20					25					30		
Pro	Leu	Phe	Ser	Asp	Thr	Gln	Pro	Arg	Leu	Gln	Phe	Ala	Leu	Glu	Gln
		35					40					45			
Leu	Leu	His	Thr	Arg	Ala	Ser	Ser	Ser	Phe	Met	Leu	Ala	Lys	Ala	Pro
	50					55					60				
Glu	Glu	Ser	Glu	Tyr	Leu	Asn	Leu	Ile	Ala	Asn	Ala	Ala	Arg	Thr	Leu
65					70					75					80
Gln	Ser	Asp	Ala	Gly	Gln	Leu	Val	Gly	Gly	His	Tyr	Glu	Val	Ser	Gly
			85						90					95	
His	Ser	Ile	Arg	Leu	Arg	His	Ala	Val	Ser	Ala	Asp	Asp	Asn	Phe	Ala
			100					105					110		
Thr	Leu	Thr	Gln	Val	Val	Ala	Ala	Asp	Trp	Val	Glu	Ala	Glu	Gln	Leu
	115					120						125			
Phe	Gly	Cys	Leu	Arg	Gln	Phe	Asn	Gly	Asp	Ile	Thr	Leu	Gln	Pro	Gly
	130					135				140					
Leu	Val	His	Gln	Ala	Asn	Gly	Gly	Ile	Leu	Ile	Ile	Ser	Leu	Arg	Thr
145					150					155					160
Leu	Leu	Ala	Gln	Pro	Leu	Leu	Trp	Met	Arg	Leu	Lys	Asn	Ile	Val	Asn
			165						170					175	
Arg	Glu	Arg	Phe	Asp	Trp	Val	Ala	Phe	Asp	Glu	Ser	Arg	Pro	Leu	Pro
			180					185					190		
Val	Ser	Val	Pro	Ser	Met	Pro	Leu	Lys	Leu	Lys	Val	Ile	Leu	Val	Gly
	195					200						205			
Glu	Arg	Glu	Ser	Leu	Ala	Asp	Phe	Gln	Glu	Met	Glu	Pro	Glu	Leu	Ser
	210					215					220				
Glu	Gln	Ala	Ile	Tyr	Ser	Glu	Phe	Glu	Asp	Thr	Leu	Gln	Ile	Val	Asp
225					230					235					240
Ala	Glu	Ser	Val	Thr	Gln	Trp	Cys	Arg	Trp	Val	Thr	Phe	Thr	Ala	Arg
			245						250					255	
His	Asn	His	Leu	Pro	Ala	Pro	Gly	Ala	Asp	Ala	Trp	Pro	Ile	Leu	Ile
			260				265						270		
Arg	Glu	Ala	Arg	Tyr	Thr	Gly	Glu	Gln	Glu	Thr	Leu	Pro	Leu	Ser	
	275					280						285			

Pro Gln Trp Ile Leu Arg Gln Cys Lys Glu Val Ala Ser Leu Cys Asp
 290 295 300
 Gly Asp Thr Phe Ser Gly Glu Gln Leu Asn Leu Met Leu Gln Gln Arg
 305 310 315 320
 Glu Trp Arg Glu Gly Phe Leu Ala Glu Arg Met Gln Asp Glu Ile Leu
 325 330 335
 Gln Glu Gln Ile Leu Ile Glu Thr Glu Gly Glu Arg Ile Gly Gln Ile
 340 345 350
 Asn Ala Leu Ser Val Ile Glu Phe Pro Gly His Pro Arg Ala Phe Gly
 355 360 365
 Glu Pro Ser Arg Ile Ser Cys Val Val His Ile Gly Asp Gly Glu Phe
 370 375 380
 Thr Asp Ile Glu Arg Lys Ala Glu Leu Gly Gly Asn Ile His Ala Lys
 385 390 395 400
 Gly Met Met Ile Met Gln Ala Phe Leu Met Ser Glu Leu Gln Leu Glu
 405 410 415
 Gln Gln Ile Pro Phe Ser Ala Ser Leu Thr Phe Glu Gln Ser Tyr Ser
 420 425 430
 Glu Val Asp Gly Asp Ser Ala Ser Met Ala Glu Leu Cys Ala Leu Ile
 435 440 445
 Ser Ala Leu Ala Asp Val Pro Val Asn Gln Ser Ile Ala Ile Thr Gly
 450 455 460
 Ser Val Asp Gln Phe Gly Arg Ala Gln Pro Val Gly Gly Leu Asn Glu
 465 470 475 480
 Lys Ile Glu Gly Phe Phe Ala Ile Cys Gln Gln Arg Glu Leu Thr Gly
 485 490 495
 Lys Gln Gly Val Ile Ile Pro Thr Ala Asn Val Arg His Leu Ser Leu
 500 505 510
 His Ser Glu Leu Val Lys Ala Val Glu Glu Gly Lys Phe Thr Ile Trp
 515 520 525
 Ala Val Asp Asp Val Thr Asp Ala Leu Pro Leu Leu Leu Asn Leu Val
 530 535 540
 Trp Asp Gly Glu Gly Gln Thr Thr Leu Met Gln Thr Ile Gln Glu Arg
 545 550 555 560
 Ile Ala Gln Ala Ser Gln Gln Glu Gly Arg His Arg Phe Pro Trp Pro
 565 570 575
 Leu Arg Trp Leu Asn Trp Phe Ile Pro Asn
 580 585

<210> 247

<211> 394

<212> PRT

<213> E. Coli

<400> 247

Met Ser Lys Glu Lys Phe Glu Arg Thr Lys Pro His Val Asn Val Gly
 1 5 10 15
 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
 20 25 30
 Thr Thr Val Leu Ala Lys Thr Tyr Gly Gly Ala Ala Arg Ala Phe Asp
 35 40 45
 Gln Ile Asp Asn Ala Pro Glu Lys Ala Arg Gly Ile Thr Ile Asn
 50 55 60
 Thr Ser His Val Glu Tyr Asp Thr Pro Thr Arg His Tyr Ala His Val
 65 70 75 80
 Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala

65					70					75				80
Pro	His	Arg	Ile	Asn	Ile	Ile	Asp	Thr	Pro	Gly	His	Val	Asp	Thr
				85					90				95	
Ile	Glu	Val	Glu	Arg	Ser	Met	Arg	Val	Leu	Asp	Gly	Ala	Val	Met
			100					105					110	
Tyr	Cys	Ala	Val	Gly	Gly	Val	Gln	Pro	Gln	Ser	Glu	Thr	Val	Trp
		115					120					125		Arg
Gln	Ala	Asn	Lys	Tyr	Lys	Val	Pro	Arg	Ile	Ala	Phe	Val	Asn	Lys
		130				135					140			Met
Asp	Arg	Met	Gly	Ala	Asn	Phe	Leu	Lys	Val	Val	Asn	Gln	Ile	Lys
145					150					155				160
Arg	Leu	Gly	Ala	Asn	Pro	Val	Pro	Leu	Gln	Leu	Ala	Ile	Gly	Ala
			165						170					175
Glu	His	Phe	Thr	Gly	Val	Val	Asp	Leu	Val	Lys	Met	Lys	Ala	Ile
			180					185					190	Asn
Trp	Asn	Asp	Ala	Asp	Gln	Gly	Val	Thr	Phe	Glu	Tyr	Glu	Asp	Ile
		195					200					205		Pro
Ala	Asp	Met	Val	Glu	Leu	Ala	Asn	Glu	Trp	His	Gln	Asn	Leu	Ile
		210				215					220			Glu
Ser	Ala	Ala	Glu	Ala	Ser	Glu	Glu	Leu	Met	Glu	Lys	Tyr	Leu	Gly
225					230					235				240
Glu	Glu	Leu	Thr	Glu	Ala	Glu	Ile	Lys	Gly	Ala	Leu	Arg	Gln	Arg
			245						250					255
Leu	Asn	Asn	Glu	Ile	Ile	Leu	Val	Thr	Cys	Gly	Ser	Ala	Phe	Lys
			260					265					270	Asn
Lys	Gly	Val	Gln	Ala	Met	Leu	Asp	Ala	Val	Ile	Asp	Tyr	Leu	Pro
		275					280					285		Ser
Pro	Val	Asp	Val	Pro	Ala	Ile	Asn	Gly	Ile	Leu	Asp	Asp	Gly	Lys
		290				295					300			Asp
Thr	Pro	Ala	Glu	Arg	His	Ala	Ser	Asp	Asp	Glu	Pro	Phe	Ser	Ala
305					310					315				320
Ala	Phe	Lys	Ile	Ala	Thr	Asp	Pro	Phe	Val	Gly	Asn	Leu	Thr	Phe
			325						330					335
Arg	Val	Tyr	Ser	Gly	Val	Val	Asn	Ser	Gly	Asp	Thr	Val	Leu	Asn
			340					345					350	Ser
Val	Lys	Ala	Ala	Arg	Glu	Arg	Phe	Gly	Arg	Ile	Val	Gln	Met	His
		355					360					365		Ala
Asn	Lys	Arg	Glu	Glu	Ile	Lys	Glu	Val	Arg	Ala	Gly	Asp	Ile	Ala
		370				375					380			Ala
Ala	Ile	Gly	Leu	Lys	Asp	Val	Thr	Thr	Gly	Asp	Thr	Leu	Cys	Asp
385					390				395					400
Asp	Ala	Pro	Ile	Ile	Leu	Glu	Arg	Met	Glu	Phe	Pro	Glu	Pro	Val
			405						410					415
Ser	Ile	Ala	Val	Glu	Pro	Lys	Thr	Lys	Ala	Asp	Gln	Glu	Lys	Met
			420					425					430	Gly
Leu	Ala	Leu	Gly	Arg	Leu	Ala	Lys	Glu	Asp	Pro	Ser	Phe	Arg	Val
		435					440					445		Trp
Thr	Asp	Glu	Glu	Ser	Asn	Gln	Thr	Ile	Ile	Ala	Gly	Met	Gly	Glu
		450				455					460			Leu
His	Leu	Asp	Ile	Ile	Val	Asp	Arg	Met	Lys	Arg	Glu	Phe	Asn	Val
465					470				475					480
Ala	Asn	Val	Gly	Lys	Pro	Gln	Val	Ala	Tyr	Arg	Glu	Thr	Ile	Arg
			485						490					495
Lys	Val	Thr	Asp	Val	Glu	Gly	Lys	His	Ala	Lys	Gln	Ser	Gly	Gly
		500						505					510	Arg
Gly	Gln	Tyr	Gly	His	Val	Val	Ile	Asp	Met	Tyr	Pro	Leu	Glu	Pro
		515					520					525		Gly

Ser Asn Pro Lys Gly Tyr Glu Phe Ile Asn Asp Ile Lys Gly Gly Val
 530 535 540
 Ile Pro Gly Glu Tyr Ile Pro Ala Val Asp Lys Gly Ile Gln Glu Gln
 545 550 555 560
 Leu Lys Ala Gly Pro Leu Ala Gly Tyr Pro Val Val Asp Met Gly Ile
 565 570 575
 Arg Leu His Phe Gly Ser Tyr His Asp Val Asp Ser Ser Glu Leu Ala
 580 585 590
 Phe Lys Leu Ala Ala Ser Ile Ala Phe Lys Glu Gly Phe Lys Lys Ala
 595 600 605
 Lys Pro Val Leu Leu Glu Pro Ile Met Lys Val Glu Val Glu Thr Pro
 610 615 620
 Glu Glu Asn Thr Gly Asp Val Ile Gly Asp Leu Ser Arg Arg Arg Gly
 625 630 635 640
 Met Leu Lys Gly Gln Glu Ser Glu Val Thr Gly Val Lys Ile His Ala
 645 650 655
 Glu Val Pro Leu Ser Glu Met Phe Gly Tyr Ala Thr Gln Leu Arg Ser
 660 665 670
 Leu Thr Lys Gly Arg Ala Ser Tyr Thr Met Glu Phe Leu Lys Tyr Asp
 675 680 685
 Glu Ala Pro Ser Asn Val Ala Gln Ala Val Ile Glu Ala Arg Gly Lys
 690 695 700

<210> 249

<211> 179

<212> PRT

<213> E. Coli

<400> 249

Met Pro Arg Arg Arg Val Ile Gly Gln Arg Lys Ile Leu Pro Asp Pro
 1 5 10 15
 Lys Phe Gly Ser Glu Leu Leu Ala Lys Phe Val Asn Ile Leu Met Val
 20 25 30
 Asp Gly Lys Lys Ser Thr Ala Glu Ser Ile Val Tyr Ser Ala Leu Glu
 35 40 45
 Thr Leu Ala Gln Arg Ser Gly Lys Ser Glu Leu Glu Ala Phe Glu Val
 50 55 60
 Ala Leu Glu Asn Val Arg Pro Thr Val Glu Val Lys Ser Arg Arg Val
 65 70 75 80
 Gly Gly Ser Thr Tyr Gln Val Pro Val Glu Val Arg Pro Val Arg Arg
 85 90 95
 Asn Ala Leu Ala Met Arg Trp Ile Val Glu Ala Ala Arg Lys Arg Gly
 100 105 110
 Asp Lys Ser Met Ala Leu Arg Leu Ala Asn Glu Leu Ser Asp Ala Ala
 115 120 125
 Glu Asn Lys Gly Thr Ala Val Lys Lys Arg Glu Asp Val His Arg Met
 130 135 140
 Ala Glu Ala Asn Lys Ala Phe Ala His Tyr Arg Trp Leu Ser Leu Arg
 145 150 155 160
 Ser Phe Ser His Gln Ala Gly Ala Ser Ser Lys Gln Pro Ala Leu Gly
 165 170 175
 Tyr Leu Asn

<210> 250

<211> 124
 <212> PRT
 <213> E. Coli

<400> 250
 Met Ala Thr Val Asn Gln Leu Val Arg Lys Pro Arg Ala Arg Lys Val
 1 5 10 15
 Ala Lys Ser Asn Val Pro Ala Leu Glu Ala Cys Pro Gln Lys Arg Gly
 20 25 30
 Val Cys Thr Arg Val Tyr Thr Thr Pro Lys Lys Pro Asn Ser Ala
 35 40 45
 Leu Arg Lys Val Cys Arg Val Arg Leu Thr Asn Gly Phe Glu Val Thr
 50 55 60
 Ser Tyr Ile Gly Gly Glu Gly His Asn Leu Gln Glu His Ser Val Ile
 65 70 75 80
 Leu Ile Arg Gly Gly Arg Val Lys Asp Leu Pro Gly Val Arg Tyr His
 85 90 95
 Thr Val Arg Gly Ala Leu Asp Cys Ser Gly Val Lys Asp Arg Lys Gln
 100 105 110
 Ala Arg Ser Lys Tyr Gly Val Lys Arg Pro Lys Ala
 115 120

<210> 251
 <211> 165
 <212> PRT
 <213> E. Coli

<400> 251
 Met Ala Leu Asn Leu Gln Asp Lys Gln Ala Ile Val Ala Glu Val Ser
 1 5 10 15
 Glu Val Ala Lys Gly Ala Leu Ser Ala Val Val Ala Asp Ser Arg Gly
 20 25 30
 Val Thr Val Asp Lys Met Thr Glu Leu Arg Lys Ala Gly Arg Glu Ala
 35 40 45
 Gly Val Tyr Met Arg Val Val Arg Asn Thr Leu Leu Arg Arg Ala Val
 50 55 60
 Glu Gly Thr Pro Phe Glu Cys Leu Lys Asp Ala Phe Val Gly Pro Thr
 65 70 75 80
 Leu Ile Ala Tyr Ser Met Glu His Pro Gly Ala Ala Ala Arg Leu Phe
 85 90 95
 Lys Glu Phe Ala Lys Ala Asn Ala Lys Phe Glu Val Lys Ala Ala Ala
 100 105 110
 Phe Glu Gly Glu Leu Ile Pro Ala Ser Gln Ile Asp Arg Leu Ala Thr
 115 120 125
 Leu Pro Thr Tyr Glu Glu Ala Ile Ala Arg Leu Met Ala Thr Met Lys
 130 135 140
 Glu Ala Ser Ala Gly Lys Leu Val Arg Thr Leu Ala Ala Val Arg Asp
 145 150 155 160
 Ala Lys Glu Ala Ala
 165

<210> 252
 <211> 121
 <212> PRT
 <213> E. Coli

<400> 252

Met	Ser	Ile	Thr	Lys	Asp	Gln	Ile	Ile	Glu	Ala	Val	Ala	Ala	Met	Ser
1				5					10					15	
Val	Met	Asp	Val	Val	Glu	Leu	Ile	Ser	Ala	Met	Glu	Glu	Lys	Phe	Gly
			20					25					30		
Val	Ser	Ala	Ala	Ala	Ala	Val	Ala	Val	Ala	Ala	Gly	Pro	Val	Glu	Ala
		35					40					45			
Ala	Glu	Glu	Lys	Thr	Glu	Phe	Asp	Val	Ile	Leu	Lys	Ala	Ala	Gly	Ala
	50					55					60				
Asn	Lys	Val	Ala	Val	Ile	Lys	Ala	Val	Arg	Gly	Ala	Thr	Gly	Leu	Gly
65					70					75				80	
Leu	Lys	Glu	Ala	Lys	Asp	Leu	Val	Glu	Ser	Ala	Pro	Ala	Ala	Leu	Lys
				85				90						95	
Glu	Gly	Val	Ser	Lys	Asp	Asp	Ala	Glu	Ala	Leu	Lys	Lys	Ala	Leu	Glu
			100					105					110		
Glu	Ala	Gly	Ala	Glu	Val	Glu	Val	Lys							
		115						120							

<210> 253

<211> 714

<212> PRT

<213> E. Coli

<400> 253

Met	Ser	Arg	Ile	Ile	Met	Leu	Ile	Pro	Thr	Gly	Thr	Ser	Val	Gly	Leu
1				5					10					15	
Thr	Ser	Val	Ser	Leu	Gly	Val	Ile	Arg	Ala	Met	Glu	Arg	Lys	Gly	Val
			20					25					30		
Arg	Leu	Ser	Val	Phe	Lys	Pro	Ile	Ala	Gln	Pro	Arg	Thr	Gly	Gly	Asp
		35					40					45			
Ala	Pro	Asp	Gln	Thr	Thr	Thr	Ile	Val	Arg	Ala	Asn	Ser	Ser	Thr	Thr
	50					55					60				
Thr	Ala	Ala	Glu	Pro	Leu	Lys	Met	Ser	Tyr	Val	Glu	Gly	Leu	Leu	Ser
65					70					75				80	
Ser	Asn	Gln	Lys	Asp	Val	Leu	Met	Glu	Glu	Ile	Val	Ala	Asn	Tyr	His
			85					90						95	
Ala	Asn	Thr	Lys	Asp	Ala	Glu	Val	Val	Leu	Val	Glu	Gly	Leu	Val	Pro
			100					105					110		
Thr	Arg	Lys	His	Gln	Phe	Ala	Gln	Ser	Leu	Asn	Tyr	Glu	Ile	Ala	Lys
		115					120						125		
Thr	Leu	Asn	Ala	Glu	Ile	Val	Phe	Val	Met	Ser	Gln	Gly	Thr	Asp	Thr
	130					135						140			
Pro	Glu	Gln	Leu	Lys	Glu	Arg	Ile	Glu	Leu	Thr	Arg	Asn	Ser	Phe	Gly
145					150					155					160
Gly	Ala	Lys	Asn	Thr	Asn	Ile	Thr	Gly	Val	Ile	Val	Asn	Lys	Leu	Asn
			165					170						175	
Ala	Pro	Val	Asp	Glu	Gln	Gly	Arg	Thr	Arg	Pro	Asp	Leu	Ser	Glu	Ile
			180					185					190		
Phe	Asp	Asp	Ser	Ser	Lys	Ala	Lys	Val	Asn	Asn	Val	Asp	Pro	Ala	Lys
		195					200					205			
Leu	Gln	Glu	Ser	Ser	Pro	Leu	Pro	Val	Leu	Gly	Ala	Val	Pro	Trp	Ser
	210					215					220				
Phe	Asp	Leu	Ile	Ala	Thr	Arg	Ala	Ile	Asp	Met	Ala	Arg	His	Leu	Asn
225					230					235				240	
Ala	Thr	Ile	Ile	Asn	Glu	Gly	Asp	Ile	Asn	Thr	Arg	Arg	Val	Lys	Ser

									245							255
Val	Thr	Phe	Cys	Ala	Arg	Ser	Ile	Pro	His	Met	Leu	Glu	His	Phe	Arg	
			260					265					270			
Ala	Gly	Ser	Leu	Leu	Val	Thr	Ser	Ala	Asp	Arg	Pro	Asp	Val	Leu	Val	
		275					280					285				
Ala	Ala	Cys	Leu	Ala	Ala	Met	Asn	Gly	Val	Glu	Ile	Gly	Ala	Leu	Leu	
		290				295				300						
Leu	Thr	Gly	Gly	Tyr	Glu	Met	Asp	Ala	Arg	Ile	Ser	Lys	Leu	Cys	Glu	
305				310						315					320	
Arg	Ala	Phe	Ala	Thr	Gly	Leu	Pro	Val	Phe	Met	Val	Asn	Thr	Asn	Thr	
			325						330					335		
Trp	Gln	Thr	Ser	Leu	Ser	Leu	Gln	Ser	Phe	Asn	Leu	Glu	Val	Pro	Val	
			340					345					350			
Asp	Asp	His	Glu	Arg	Ile	Glu	Lys	Val	Gln	Glu	Tyr	Val	Ala	Asn	Tyr	
		355					360					365				
Ile	Asn	Ala	Asp	Trp	Ile	Glu	Ser	Leu	Thr	Ala	Thr	Ser	Glu	Arg	Ser	
		370				375					380					
Arg	Arg	Leu	Ser	Pro	Pro	Ala	Phe	Arg	Tyr	Gln	Leu	Thr	Glu	Leu	Ala	
385				390						395					400	
Arg	Lys	Ala	Gly	Lys	Arg	Ile	Val	Leu	Pro	Glu	Gly	Asp	Glu	Pro	Arg	
			405						410					415		
Thr	Val	Lys	Ala	Ala	Ala	Ile	Cys	Ala	Glu	Arg	Gly	Ile	Ala	Thr	Cys	
			420					425					430			
Val	Leu	Leu	Gly	Asn	Pro	Ala	Glu	Ile	Asn	Arg	Val	Ala	Ala	Ser	Gln	
		435					440					445				
Gly	Val	Glu	Leu	Gly	Ala	Gly	Ile	Glu	Ile	Val	Asp	Pro	Glu	Val	Val	
	450					455					460					
Arg	Glu	Ser	Tyr	Val	Gly	Arg	Leu	Val	Glu	Leu	Arg	Lys	Asn	Lys	Gly	
465				470						475					480	
Met	Thr	Glu	Thr	Val	Ala	Arg	Glu	Gln	Leu	Glu	Asp	Asn	Val	Val	Leu	
			485						490					495		
Gly	Thr	Leu	Met	Leu	Glu	Gln	Asp	Glu	Val	Asp	Gly	Leu	Val	Ser	Gly	
			500					505					510			
Ala	Val	His	Thr	Thr	Ala	Asn	Thr	Ile	Arg	Pro	Pro	Leu	Gln	Leu	Ile	
		515					520					525				
Lys	Thr	Ala	Pro	Gly	Ser	Ser	Leu	Val	Ser	Ser	Val	Phe	Phe	Met	Leu	
	530					535					540					
Leu	Pro	Glu	Gln	Val	Tyr	Val	Tyr	Gly	Asp	Cys	Ala	Ile	Asn	Pro	Asp	
545				550						555					560	
Pro	Thr	Ala	Glu	Gln	Leu	Ala	Glu	Ile	Ala	Ile	Gln	Ser	Ala	Asp	Ser	
			565						570					575		
Ala	Ala	Ala	Phe	Gly	Ile	Glu	Pro	Arg	Val	Ala	Met	Leu	Ser	Tyr	Ser	
			580			</										

Leu Thr Ala Ile Gln Ser Ala Gln Gln Gln
705 710

<210> 254
<211> 588
<212> PRT
<213> E. Coli

<400> 254
Met Asn Asn Ser Ile Asn His Lys Phe His His Ile Ser Arg Ala Glu
1 5 10 15
Tyr Gln Glu Leu Leu Ala Val Ser Arg Gly Asp Ala Val Ala Asp Tyr
20 25 30
Ile Ile Asp Asn Val Ser Ile Leu Asp Leu Ile Asn Gly Gly Glu Ile
35 40 45
Ser Gly Pro Ile Val Ile Lys Gly Arg Tyr Ile Ala Gly Val Gly Ala
50 55 60
Glu Tyr Thr Asp Ala Pro Ala Leu Gln Arg Ile Asp Ala Arg Gly Ala
65 70 75 80
Thr Ala Val Pro Gly Phe Ile Asp Ala His Leu His Ile Glu Ser Ser
85 90 95
Met Met Thr Pro Val Thr Phe Glu Thr Ala Thr Leu Pro Arg Gly Leu
100 105 110
Thr Thr Val Ile Cys Asp Pro His Glu Ile Val Asn Val Met Gly Glu
115 120 125
Ala Gly Phe Ala Trp Phe Ala Arg Cys Ala Glu Gln Ala Arg Gln Asn
130 135 140
Gln Tyr Leu Gln Val Ser Ser Cys Val Pro Ala Leu Glu Gly Cys Asp
145 150 155 160
Val Asn Gly Ala Ser Phe Thr Leu Glu Gln Met Leu Ala Trp Arg Asp
165 170 175
His Pro Gln Val Thr Gly Leu Ala Glu Met Met Asp Tyr Pro Gly Val
180 185 190
Ile Ser Gly Gln Asn Ala Leu Leu Asp Lys Leu Asp Ala Phe Arg His
195 200 205
Leu Thr Leu Asp Gly His Cys Pro Gly Leu Gly Gly Lys Glu Leu Asn
210 215 220
Ala Tyr Ile Thr Ala Gly Ile Glu Asn Cys His Glu Ser Tyr Gln Leu
225 230 235 240
Glu Glu Gly Arg Arg Lys Leu Gln Leu Gly Met Ser Leu Met Ile Arg
245 250 255
Glu Gly Ser Ala Ala Arg Asn Leu Asn Ala Leu Ala Pro Leu Ile Asn
260 265 270
Glu Phe Asn Ser Pro Gln Cys Met Leu Cys Thr Asp Asp Arg Asn Pro
275 280 285
Trp Glu Ile Ala His Glu Gly His Ile Asp Ala Leu Ile Arg Arg Leu
290 295 300
Ile Glu Gln His Asn Val Pro Leu His Val Ala Tyr Arg Val Ala Ser
305 310 315 320
Trp Ser Thr Ala Arg His Phe Gly Leu Asn His Leu Gly Leu Leu Ala
325 330 335
Pro Gly Lys Gln Ala Asp Ile Val Leu Leu Ser Asp Ala Arg Lys Val
340 345 350
Thr Val Gln Gln Val Leu Val Lys Gly Glu Pro Ile Asp Ala Gln Thr
355 360 365
Leu Gln Ala Glu Glu Ser Ala Arg Leu Ala Gln Ser Ala Pro Pro Tyr

370		375		380
Gly Asn Thr Ile Ala Arg	Gln Pro Val Ser	Ala Ser Asp Phe Ala Leu		
385		390	395	400
Gln Phe Thr Pro Gly Lys Arg Tyr Arg	Val Ile Asp Val Ile His Asn			
	405	410	415	
Glu Leu Ile Thr His Ser His Ser	Ser Val Tyr Ser Glu Asn Gly Phe			
	420	425	430	
Asp Arg Asp Asp Val Ser Phe Ile Ala Val Leu Glu Arg Tyr Gly Gln		445		
	435	440		
Arg Leu Ala Pro Ala Cys Gly Leu Leu Gly Gly Phe Gly Leu Asn Glu		460		
	450	455		
Gly Ala Leu Ala Ala Thr Val Ser His Asp Ser His Asn Ile Val Val		475		
465	470			480
Ile Gly Arg Ser Ala Glu Glu Met Ala Leu Ala Val Asn Gln Val Ile		490		495
	485			
Gln Asp Gly Gly Gly Leu Cys Val Val Arg Asn Gly Gln Val Gln Ser		505		510
	500			
His Leu Pro Leu Pro Ile Ala Gly Leu Met Ser Thr Asp Thr Ala Gln		520		525
	515			
Ser Leu Ala Glu Gln Ile Asp Ala Leu Lys Ala Ala Ala Arg Glu Cys		535		540
	530			
Gly Pro Leu Pro Asp Glu Pro Phe Ile Gln Met Ala Phe Leu Ser Leu		555		560
545	550			
Pro Val Ile Pro Ala Leu Lys Leu Thr Ser Gln Gly Leu Phe Asp Gly		570		575
	565			
Glu Lys Phe Ala Phe Thr Thr Leu Glu Val Thr Glu		585		
	580			

<210> 255
 <211> 408
 <212> PRT
 <213> E. Coli

<400> 255
Met Ala Tyr Cys Asn Pro Gly Leu Glu Ser Arg Pro Asn Lys Arg Asn
1 5 10 15
Ala Leu Arg Arg His Val Val Thr Gly Ile Gly Met Lys Ile Val Ile
20 25 30
Ala Pro Asp Ser Tyr Lys Glu Ser Leu Ser Ala Ser Glu Val Ala Gln
35 40 45
Ala Ile Glu Lys Gly Phe Arg Glu Ile Phe Pro Asp Ala Gln Tyr Val
50 55 60
Ser Val Pro Val Ala Asp Gly Gly Glu Gly Thr Val Glu Ala Met Ile
65 70 75 80
Ala Ala Thr Gln Gly Ala Glu Arg His Ala Trp Val Thr Gly Pro Leu
85 90 95
Gly Glu Lys Val Asn Ala Ser Trp Gly Ile Ser Gly Asp Gly Lys Thr
100 105 110
Ala Phe Ile Glu Met Ala Ala Ala Ser Gly Leu Glu Leu Val Pro Ala
115 120 125
Glu Lys Arg Asp Pro Leu Val Thr Thr Ser Arg Gly Thr Gly Glu Leu
130 135 140
Ile Leu Gln Ala Leu Glu Ser Gly Ala Thr Asn Ile Ile Ile Gly Ile
145 150 155 160
Gly Gly Ser Ala Thr Asn Asp Gly Gly Ala Gly Met Val Gln Ala Leu
165 170 175

145					150				155				160
Ser	Val	Val	His	Thr	Gly	Glu	Ile	Gly	Ala	Gly	Asn	Val	Thr
				165					170				175
Ala	Asn	Gln	Val	Ile	Val	Ala	Leu	Asn	Ile	Ala	Ala	Met	Ser
			180					185				190	
Leu	Thr	Leu	Ala	Thr	Lys	Ala	Gly	Val	Asn	Pro	Asp	Leu	Val
		195					200					205	
Ala	Ile	Arg	Gly	Gly	Leu	Ala	Gly	Ser	Thr	Val	Leu	Asp	Ala
	210					215					220		
Pro	Met	Val	Met	Asp	Arg	Asn	Phe	Lys	Pro	Gly	Phe	Arg	Ile
225				230						235			240
His	Ile	Lys	Asp	Leu	Ala	Asn	Ala	Leu	Asp	Thr	Ser	His	Gly
			245						250				255
Ala	Gln	Leu	Pro	Leu	Thr	Ala	Ala	Val	Met	Glu	Met	Met	Gln
		260					265						270
Arg	Ala	Asp	Gly	Leu	Gly	Thr	Ala	Asp	His	Ser	Ala	Leu	Ala
		275				280						285	
Tyr	Glu	Lys	Leu	Ala	Lys	Val	Glu	Val	Thr	Arg			
	290					295							

<210> 257

<211> 256

<212> PRT

<213> E. Coli

<400> 257

Met	Asn	Asn	Asp	Val	Phe	Pro	Asn	Lys	Phe	Lys	Ala	Ala	Leu	Ala	Ala
1				5					10					15	
Lys	Gln	Val	Gln	Ile	Gly	Cys	Trp	Ser	Ala	Leu	Ser	Asn	Pro	Ile	Ser
			20					25					30		
Thr	Glu	Val	Leu	Gly	Leu	Ala	Gly	Phe	Asp	Trp	Leu	Val	Leu	Asp	Gly
		35					40					45			
Glu	His	Ala	Pro	Asn	Asp	Ile	Ser	Thr	Phe	Ile	Pro	Gln	Leu	Met	Ala
	50					55				60					
Leu	Lys	Gly	Ser	Ala	Ser	Ala	Pro	Val	Val	Arg	Val	Pro	Thr	Asn	Glu
65					70					75					80
Pro	Val	Ile	Ile	Lys	Arg	Leu	Leu	Asp	Ile	Gly	Phe	Tyr	Asn	Phe	Leu
				85					90					95	
Ile	Pro	Phe	Val	Glu	Thr	Lys	Glu	Glu	Ala	Glu	Leu	Ala	Val	Ala	Ser
			100					105					110		
Thr	Arg	Tyr	Pro	Pro	Glu	Gly	Ile	Arg	Gly	Val	Ser	Val	Ser	His	Arg
		115					120						125		
Ala	Asn	Met	Phe	Gly	Thr	Val	Ala	Asp	Tyr	Phe	Ala	Gln	Ser	Asn	Lys
	130					135					140				
Asn	Ile	Thr	Ile	Leu	Val	Gln	Ile	Glu	Ser	Gln	Gln	Gly	Val	Asp	Asn
145				150						155					160
Val	Asp	Ala	Ile	Ala	Ala	Thr	Glu	Gly	Val	Asp	Gly	Ile	Phe	Val	Gly
			165						170					175	
Pro	Ser	Asp	Leu	Ala	Ala	Ala	Leu	Gly	His	Leu	Gly	Asn	Ala	Ser	His
		180						185					190		
Pro	Asp	Val	Gln	Lys	Ala	Ile	Gln	His	Ile	Phe	Asn	Arg	Ala	Ser	Ala
	195						200					205			
His	Gly	Lys	Pro	Ser	Gly	Ile	Leu	Ala	Pro	Val	Glu	Ala	Asp	Ala	Arg
	210					215					220				
Arg	Tyr	Leu	Glu	Trp	Gly	Ala	Thr	Phe	Val	Ala	Val	Gly	Ser	Asp	Leu

225		230		235		240									
Gly	Val	Phe	Arg	Ser	Ala	Thr	Gln	Lys	Leu	Ala	Asp	Thr	Phe	Lys	Lys
				245					250					255	

<210> 258
 <211> 444
 <212> PRT
 <213> E. Coli

<400> 258															
Met	Ile	Leu	Asp	Thr	Val	Asp	Glu	Lys	Lys	Lys	Gly	Val	His	Thr	Arg
1				5					10					15	
Tyr	Leu	Ile	Leu	Leu	Ile	Ile	Phe	Ile	Val	Thr	Ala	Val	Asn	Tyr	Ala
			20					25					30		
Asp	Arg	Ala	Thr	Leu	Ser	Ile	Ala	Gly	Thr	Glu	Val	Ala	Lys	Glu	Leu
		35					40					45			
Gln	Leu	Ser	Ala	Val	Ser	Met	Gly	Tyr	Ile	Phe	Ser	Ala	Phe	Gly	Trp
50					55					60					
Ala	Tyr	Leu	Leu	Met	Gln	Ile	Pro	Gly	Gly	Trp	Leu	Leu	Asp	Lys	Phe
65				70					75					80	
Gly	Ser	Lys	Lys	Val	Tyr	Thr	Tyr	Ser	Leu	Phe	Phe	Trp	Ser	Leu	Phe
			85					90					95		
Thr	Phe	Leu	Gln	Gly	Phe	Val	Asp	Met	Phe	Pro	Leu	Ala	Trp	Ala	Gly
			100					105					110		
Ile	Ser	Met	Phe	Phe	Met	Arg	Phe	Met	Leu	Gly	Phe	Ser	Glu	Ala	Pro
		115					120					125			
Ser	Phe	Pro	Ala	Asn	Ala	Arg	Ile	Val	Ala	Ala	Trp	Phe	Pro	Thr	Lys
130						135					140				
Glu	Arg	Gly	Thr	Ala	Ser	Ala	Ile	Phe	Asn	Ser	Ala	Gln	Tyr	Phe	Ser
145				150					155					160	
Leu	Ala	Leu	Phe	Ser	Pro	Leu	Leu	Gly	Trp	Leu	Thr	Phe	Ala	Trp	Gly
			165					170					175		
Trp	Glu	His	Val	Phe	Thr	Val	Met	Gly	Val	Ile	Gly	Phe	Val	Leu	Thr
			180					185					190		
Ala	Leu	Trp	Ile	Lys	Leu	Ile	His	Asn	Pro	Thr	Asp	His	Pro	Arg	Met
		195					200				205				
Ser	Ala	Glu	Glu	Leu	Lys	Phe	Ile	Ser	Glu	Asn	Gly	Ala	Val	Val	Asp
210					215					220					
Met	Asp	His	Lys	Lys	Pro	Gly	Ser	Ala	Ala	Ala	Ser	Gly	Pro	Lys	Leu
225					230					235				240	
His	Tyr	Ile	Lys	Gln	Leu	Leu	Ser	Asn	Arg	Met	Met	Leu	Gly	Val	Phe
			245					250					255		
Phe	Gly	Gln	Tyr	Phe	Ile	Asn	Thr	Ile	Thr	Trp	Phe	Phe	Leu	Thr	Trp
		260					265						270		
Phe	Pro	Ile	Tyr	Leu	Val	Gln	Glu	Lys	Gly	Met	Ser	Ile	Leu	Lys	Val
		275					280					285			
Gly	Leu	Val	Ala	Ser	Ile	Pro	Ala	Leu	Cys	Gly	Phe	Ala	Gly	Gly	Val
		290				295				300					
Leu	Gly	Gly	Val	Phe	Ser	Asp	Tyr	Leu	Ile	Lys	Arg	Gly	Leu	Ser	Leu
305					310					315				320	
Thr	Leu	Ala	Arg	Lys	Leu	Pro	Ile	Val	Leu	Gly	Met	Leu	Leu	Ala	Ser
			325					330					335		
Thr	Ile	Ile	Leu	Cys	Asn	Tyr	Thr	Asn	Asn	Thr	Thr	Leu	Val	Val	Met
			340				345					350			
Leu	Met	Ala	Leu	Ala	Phe	Phe	Gly	Lys	Gly	Phe	Gly	Ala	Leu	Gly	Trp
		355					360					365			

Pro	Val	Ile	Ser	Asp	Thr	Ala	Pro	Lys	Glu	Ile	Val	Gly	Leu	Cys	Gly
370						375					380				
Gly	Val	Phe	Asn	Val	Phe	Gly	Asn	Val	Ala	Ser	Ile	Val	Thr	Pro	Leu
385						390				395					400
Val	Ile	Gly	Tyr	Leu	Val	Ser	Glu	Leu	His	Ser	Phe	Asn	Ala	Ala	Leu
				405					410					415	
Val	Phe	Val	Gly	Cys	Ser	Ala	Leu	Met	Ala	Met	Val	Cys	Tyr	Leu	Phe
			420					425					430		
Val	Val	Gly	Asp	Ile	Lys	Arg	Met	Glu	Leu	Gln	Lys				
		435					440								

<210> 259
 <211> 511
 <212> PRT
 <213> E. Coli

<400> 259															
Met	Gln	Thr	Ser	Asp	Thr	Arg	Ala	Leu	Pro	Leu	Leu	Cys	Ala	Arg	Ser
1				5					10					15	
Val	Tyr	Lys	Gln	Tyr	Ser	Gly	Val	Asn	Val	Leu	Lys	Gly	Ile	Asp	Phe
		20						25					30		
Thr	Leu	His	Gln	Gly	Glu	Val	His	Ala	Leu	Leu	Gly	Gly	Asn	Gly	Ala
		35					40					45			
Gly	Lys	Ser	Thr	Leu	Met	Lys	Ile	Ile	Ala	Gly	Ile	Thr	Pro	Ala	Asp
	50					55					60				
Ser	Gly	Thr	Leu	Glu	Ile	Glu	Gly	Asn	Asn	Tyr	Val	Arg	Leu	Thr	Pro
65				70						75					80
Val	His	Ala	His	Gln	Leu	Gly	Ile	Tyr	Leu	Val	Pro	Gln	Glu	Pro	Leu
			85						90					95	
Leu	Phe	Pro	Ser	Leu	Ser	Ile	Lys	Glu	Asn	Ile	Leu	Phe	Gly	Leu	Ala
			100					105					110		
Lys	Lys	Gln	Leu	Ser	Met	Gln	Lys	Met	Lys	Asn	Leu	Leu	Ala	Ala	Leu
		115					120					125			
Gly	Cys	Gln	Phe	Asp	Leu	His	Ser	Leu	Ala	Gly	Ser	Leu	Asp	Val	Ala
	130					135					140				
Asp	Arg	Gln	Met	Val	Glu	Ile	Leu	Arg	Gly	Leu	Met	Arg	Asp	Ser	Arg
145				150						155					160
Ile	Leu	Ile	Leu	Asp	Glu	Pro	Thr	Ala	Ser	Leu	Thr	Pro	Ala	Glu	Thr
			165					170						175	
Glu	Arg	Leu	Phe	Ser	Arg	Leu	Gln	Glu	Leu	Leu	Ala	Thr	Gly	Val	Gly
		180						185					190		
Ile	Val	Phe	Ile	Ser	His	Lys	Leu	Pro	Glu	Ile	Arg	Gln	Ile	Ala	Asp
		195					200					205			
Arg	Ile	Ser	Val	Met	Arg	Asp	Gly	Thr	Ile	Ala	Leu	Ser	Gly	Lys	Thr
	210					215					220				
Ser	Glu	Leu	Ser	Thr	Asp	Asp	Ile	Ile	Gln	Ala	Ile	Thr	Pro	Ala	Val
225				230						235					240
Arg	Glu	Lys	Ser	Leu	Ser	Ala	Ser	Gln	Lys	Leu	Trp	Leu	Glu	Leu	Pro
			245						250					255	
Gly	Asn	Arg	Pro	Gln	His	Ala	Ala	Gly	Thr	Pro	Val	Leu	Thr	Leu	Glu
			260					265					270		
Asn	Leu	Thr	Gly	Glu	Gly	Phe	Arg	Asn	Val	Ser	Leu	Thr	Leu	Asn	Ala
	275					280						285			
Gly	Glu	Ile	Leu	Gly	Leu	Ala	Gly	Leu	Val	Gly	Ala	Gly	Arg	Thr	Glu
	290					295				300					
Leu	Ala	Glu	Thr	Leu	Tyr	Gly	Leu	Arg	Thr	Leu	Arg	Gly	Gly	Arg	Ile

305					310					315				320
Met	Leu	Asn	Gly	Lys	Glu	Ile	Asn	Lys	Leu	Ser	Thr	Gly	Glu	Arg
				325					330					335
Leu	Arg	Gly	Leu	Val	Tyr	Leu	Pro	Glu	Asp	Arg	Gln	Ser	Ser	Gly
			340					345					350	
Asn	Leu	Asp	Ala	Ser	Leu	Ala	Trp	Asn	Val	Cys	Ala	Leu	Thr	His
		355					360					365		Asn
Leu	Arg	Gly	Phe	Trp	Ala	Lys	Thr	Ala	Lys	Asp	Asn	Ala	Thr	Leu
	370					375					380			Glu
Arg	Tyr	Arg	Arg	Ala	Leu	Asn	Ile	Lys	Phe	Asn	Gln	Pro	Glu	Gln
385					390					395				400
Ala	Arg	Thr	Leu	Ser	Gly	Gly	Asn	Gln	Gln	Lys	Ile	Leu	Ile	Ala
				405					410					415
Cys	Leu	Glu	Ala	Ser	Pro	Gln	Val	Leu	Ile	Val	Asp	Glu	Pro	Thr
			420					425					430	Arg
Gly	Val	Asp	Val	Ser	Ala	Arg	Asn	Asp	Ile	Tyr	Gln	Leu	Leu	Arg
		435					440					445		Ser
Ile	Ala	Ala	Gln	Asn	Val	Ala	Val	Leu	Leu	Ile	Ser	Ser	Asp	Leu
	450					455					460			Glu
Glu	Ile	Glu	Leu	Met	Ala	Asp	Arg	Val	Tyr	Val	Met	His	Gln	Gly
465					470					475				480
Ile	Thr	His	Ser	Ala	Leu	Thr	Glu	Arg	Asp	Ile	Asn	Val	Glu	Thr
				485					490					495
Met	Arg	Val	Ala	Phe	Gly	Asp	Ser	Gln	Arg	Gln	Glu	Ala	Ser	Cys
			500					505					510	

<210> 260

<211> 342

<212> PRT

<213> E. Coli

<400> 260

Met	Leu	Lys	Phe	Ile	Gln	Asn	Asn	Arg	Glu	Ile	Thr	Ala	Leu	Leu	Ala
1				5					10					15	
Val	Val	Leu	Leu	Phe	Val	Leu	Pro	Gly	Phe	Leu	Asp	Arg	Gln	Tyr	Leu
			20					25					30		
Ser	Val	Gln	Thr	Leu	Thr	Met	Val	Tyr	Ser	Ser	Ala	Gln	Ile	Leu	Ile
		35				40						45			
Leu	Leu	Ala	Met	Gly	Ala	Thr	Leu	Val	Met	Leu	Thr	Arg	Asn	Ile	Asp
	50					55					60				
Val	Ser	Val	Gly	Ser	Ile	Thr	Gly	Met	Cys	Ala	Val	Leu	Leu	Gly	Met
65					70				75					80	
Leu	Leu	Asn	Ala	Gly	Tyr	Ser	Leu	Pro	Val	Ala	Cys	Val	Ala	Thr	Leu
				85					90					95	
Leu	Leu	Gly	Leu	Leu	Ala	Gly	Phe	Phe	Asn	Gly	Val	Leu	Val	Ala	Trp
		100						105					110		
Leu	Lys	Ile	Pro	Ala	Ile	Val	Ala	Thr	Leu	Gly	Thr	Leu	Gly	Leu	Tyr
		115					120					125			
Arg	Gly	Ile	Met	Leu	Leu	Trp	Thr	Gly	Gly	Lys	Trp	Ile	Glu	Gly	Leu
	130					135					140				
Pro	Ala	Glu	Leu	Lys	Gln	Leu	Ser	Ala	Pro	Leu	Leu	Leu	Gly	Val	Ser
145					150					155				160	
Ala	Ile	Gly	Trp	Leu	Thr	Ile	Ile	Leu	Val	Ala	Phe	Met	Ala	Trp	Leu
				165					170					175	
Leu	Ala	Lys	Thr	Ala	Phe	Gly	Arg	Ser	Phe	Tyr	Ala	Thr	Gly	Asp	Asn
			180					185						190	

Leu Gln Gly Ala Arg Gln Leu Gly Val Arg Thr Glu Ala Ile Arg Ile
 195 200 205
 Val Ala Phe Ser Leu Asn Gly Cys Met Ala Ala Leu Ala Gly Ile Val
 210 215 220
 Phe Ala Ser Gln Ile Gly Phe Ile Pro Asn Gln Thr Gly Thr Gly Leu
 225 230 235 240
 Glu Met Lys Ala Ile Ala Ala Cys Val Leu Gly Gly Ile Ser Leu Leu
 245 250 255
 Gly Gly Ser Gly Ala Ile Ile Gly Ala Val Leu Gly Ala Trp Phe Leu
 260 265 270
 Thr Gln Ile Asp Ser Val Leu Val Leu Leu Arg Ile Pro Ala Trp Trp
 275 280 285
 Asn Asp Phe Ile Ala Gly Leu Val Leu Leu Ala Val Leu Val Phe Asp
 290 295 300
 Gly Arg Leu Arg Cys Ala Leu Glu Arg Asn Leu Arg Arg Gln Lys Tyr
 305 310 315 320
 Ala Arg Phe Met Thr Pro Pro Pro Ser Val Lys Pro Ala Ser Ser Gly
 325 330 335
 Lys Lys Arg Glu Ala Ala
 340

<210> 261
 <211> 330
 <212> PRT
 <213> E. Coli

<400> 261
 Met Arg Ile Arg Tyr Gly Trp Glu Leu Ala Leu Ala Ala Leu Leu Val
 1 5 10 15
 Ile Glu Ile Val Ala Phe Gly Ala Ile Asn Pro Arg Met Leu Asp Leu
 20 25 30
 Asn Met Leu Leu Phe Ser Thr Ser Asp Phe Ile Cys Ile Gly Ile Val
 35 40 45
 Ala Leu Pro Leu Thr Met Val Ile Val Ser Gly Gly Ile Asp Ile Ser
 50 55 60
 Phe Gly Ser Thr Ile Gly Leu Cys Ala Ile Ala Leu Gly Val Leu Phe
 65 70 75 80
 Gln Ser Gly Val Pro Met Pro Leu Ala Ile Leu Leu Thr Leu Leu Leu
 85 90 95
 Gly Ala Leu Cys Gly Leu Ile Asn Ala Gly Leu Ile Ile Tyr Thr Lys
 100 105 110
 Val Asn Pro Leu Val Ile Thr Leu Gly Thr Leu Tyr Leu Phe Ala Gly
 115 120 125
 Ser Ala Leu Leu Leu Ser Gly Met Ala Gly Ala Thr Gly Tyr Glu Gly
 130 135 140
 Ile Gly Gly Phe Pro Met Ala Phe Thr Asp Phe Ala Asn Leu Asp Val
 145 150 155 160
 Leu Gly Leu Pro Val Pro Leu Ile Ile Phe Leu Ile Cys Leu Leu Val
 165 170 175
 Phe Trp Leu Trp Leu His Lys Thr His Ala Gly Arg Asn Val Phe Leu
 180 185 190
 Ile Gly Gln Ser Pro Arg Val Ala Leu Tyr Ser Ala Ile Pro Val Asn
 195 200 205
 Arg Thr Leu Cys Ala Leu Tyr Ala Met Thr Gly Leu Ala Ser Ala Val
 210 215 220
 Ala Ala Val Leu Leu Val Ser Tyr Phe Gly Ser Ala Arg Ser Asp Leu
 225 230 235 240

<210> 264
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 264
 Met His Val Thr Leu Val Glu Ile Asn Val His Glu Asp Lys Val Asp
 1 5 10 15
 Glu Phe Ile Glu Val Phe Arg Gln Asn His Leu Gly Ser Val Gln Glu
 20 25 30
 Glu Gly Asn Leu Arg Phe Asp Val Leu Gln Asp Pro Glu Val Asn Ser
 35 40 45
 Arg Phe Tyr Ile Tyr Glu Ala Tyr Lys Asp Glu Asp Ala Val Ala Phe
 50 55 60
 His Lys Thr Thr Pro His Tyr Lys Thr Cys Val Ala Lys Leu Glu Ser
 65 70 75 80
 Leu Met Thr Gly Pro Arg Lys Lys Arg Leu Phe Asn Gly Leu Met Pro
 85 90 95

<210> 265
 <211> 383
 <212> PRT
 <213> E. Coli

<400> 265
 Met Phe Glu Pro Met Glu Leu Thr Asn Asp Ala Val Ile Lys Val Ile
 1 5 10 15
 Gly Val Gly Gly Gly Gly Gly Asn Ala Val Glu His Met Val Arg Glu
 20 25 30
 Arg Ile Glu Gly Val Glu Phe Phe Ala Val Asn Thr Asp Ala Gln Ala
 35 40 45
 Leu Arg Lys Thr Ala Val Gly Gln Thr Ile Gln Ile Gly Ser Gly Ile
 50 55 60
 Thr Lys Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Asn Ala
 65 70 75 80
 Ala Asp Glu Asp Arg Asp Ala Leu Arg Ala Ala Leu Glu Gly Ala Asp
 85 90 95
 Met Val Phe Ile Ala Ala Gly Met Gly Gly Gly Thr Gly Thr Gly Ala
 100 105 110
 Ala Pro Val Val Ala Glu Val Ala Lys Asp Leu Gly Ile Leu Thr Val
 115 120 125
 Ala Val Val Thr Lys Pro Phe Asn Phe Glu Gly Lys Lys Arg Met Ala
 130 135 140
 Phe Ala Glu Gln Gly Ile Thr Glu Leu Ser Lys His Val Asp Ser Leu
 145 150 155 160
 Ile Thr Ile Pro Asn Asp Lys Leu Leu Lys Val Leu Gly Arg Gly Ile
 165 170 175
 Ser Leu Leu Asp Ala Phe Gly Ala Ala Asn Asp Val Leu Lys Gly Ala
 180 185 190
 Val Gln Gly Ile Ala Glu Leu Ile Thr Arg Pro Gly Leu Met Asn Val
 195 200 205
 Asp Phe Ala Asp Val Arg Thr Val Met Ser Glu Met Gly Tyr Ala Met
 210 215 220
 Met Gly Ser Gly Val Ala Ser Gly Glu Asp Arg Ala Glu Glu Ala Ala
 225 230 235 240
 Glu Met Ala Ile Ser Ser Pro Leu Leu Glu Asp Ile Asp Leu Ser Gly

Val	Asp	Pro	Arg	Phe	Thr	Arg	Thr	Ala	Ser	Val	Ala	Asp	Ile	Tyr	Ala		
			260					265					270				
Pro	Ile	Arg	Ser	Gly	Thr	Asp	Ile	Thr	Phe	Leu	Ser	Gly	Val	Leu	Arg		
		275					280					285					
Tyr	Leu	Ile	Glu	Asn	Asn	Lys	Ile	Asn	Ala	Glu	Tyr	Val	Lys	His	Tyr		
	290					295					300						
Thr	Asn	Ala	Ser	Leu	Leu	Val	Arg	Asp	Asp	Phe	Ala	Phe	Glu	Asp	Gly		
305					310					315					320		
Leu	Phe	Ser	Gly	Tyr	Asp	Ala	Glu	Lys	Arg	Gln	Tyr	Asp	Lys	Ser	Ser		
			325						330					335			
Trp	Asn	Tyr	Gln	Leu	Asp	Glu	Asn	Gly	Tyr	Ala	Lys	Arg	Asp	Glu	Thr		
			340					345					350				
Leu	Thr	His	Pro	Arg	Cys	Val	Trp	Asn	Leu	Leu	Lys	Glu	His	Val	Ser		
		355					360					365					
Arg	Tyr	Thr	Pro	Asp	Val	Val	Glu	Asn	Ile	Cys	Gly	Thr	Pro	Lys	Ala		
	370					375					380						
Asp	Phe	Leu	Lys	Val	Cys	Glu	Val	Leu	Ala	Ser	Thr	Ser	Ala	Pro	Asp		
385					390					395					400		
Arg	Thr	Thr	Thr	Phe	Leu	Tyr	Ala	Leu	Gly	Trp	Thr	Gln	His	Thr	Val		
				405					410					415			
Gly	Ala	Gln	Asn	Ile	Arg	Thr	Met	Ala	Met	Ile	Gln	Leu	Leu	Leu	Gly		
			420					425					430				
Asn	Met	Gly	Met	Ala	Gly	Gly	Gly	Val	Asn	Ala	Leu	Arg	Gly	His	Ser		
		435					440					445					
Asn	Ile	Gln	Gly	Leu	Thr	Asp	Leu	Gly	Leu	Leu	Ser	Thr	Ser	Leu	Pro		
	450					455					460						
Gly	Tyr	Leu	Thr	Leu	Pro	Ser	Glu	Lys	Gln	Val	Asp	Leu	Gln	Ser	Tyr		
465					470					475					480		
Leu	Glu	Ala	Asn	Thr	Pro	Lys	Ala	Thr	Leu	Ala	Asp	Gln	Val	Asn	Tyr		
				485					490					495			
Trp	Ser	Asn	Tyr	Pro	Lys	Phe	Phe	Val	Ser	Leu	Met	Lys	Ser	Phe	Tyr		
		500						505					510				
Gly	Asp	Ala	Ala	Gln	Lys	Glu	Asn	Asn	Trp	Gly	Tyr	Asp	Trp	Leu	Pro		
		515					520					525					
Lys	Trp	Asp	Gln	Thr	Tyr	Asp	Val	Ile	Lys	Tyr	Phe	Asn	Met	Met	Asp		
	530					535					540						
Glu	Gly	Lys	Val	Thr	Gly	Tyr	Phe	Cys	Gln	Gly	Phe	Asn	Pro	Val	Ala		
545					550					555					560		
Ser	Phe	Pro	Asp	Lys	Asn	Lys	Val	Val	Ser	Cys	Leu	Ser	Lys	Leu	Lys		
				565					570					575			
Tyr	Met	Val	Val	Ile	Asp	Pro	Leu	Val	Thr	Glu	Thr	Ser	Thr	Phe	Trp		
		580						585					590				
Gln	Asn	His	Gly	Glu	Ser	Asn	Asp	Val	Asp	Pro	Ala	Ser	Ile	Gln	Thr		
		595					600					605					
Glu	Val	Phe	Arg	Leu	Pro	Ser	Thr	Cys	Phe	Ala	Glu	Glu	Asp	Gly	Ser		
	610					615					620						
Ile	Ala	Asn	Ser	Gly	Arg	Trp	Leu	Gln	Trp	His	Trp	Lys	Gly	Gln	Asp		
625					630					635					640		
Ala	Pro	Gly	Glu	Ala	Arg	Asn	Asp	Gly	Glu	Ile	Leu	Ala	Gly	Ile	Tyr		
				645					650					655			
His	His	Leu	Arg	Glu	Leu	Tyr	Gln	Ser	Glu	Gly	Gly	Lys	Gly	Val	Glu		
		660						665					670				
Pro	Leu	Met	Lys	Met	Ser	Trp	Asn	Tyr	Lys	Gln	Pro	His	Glu	Pro	Gln		
		675					680					685					
Ser	Asp	Glu	Val	Ala	Lys	Glu	Asn	Asn	Gly	Tyr	Ala	Leu	Glu	Asp	Leu		
	690					695					700						
Tyr	Asp	Ala	Asn	Gly	Val	Leu	Ile	Ala	Lys	Lys	Gly	Gln	Leu	Leu	Ser		

705					710					715				720
Ser	Phe	Ala	His	Leu	Arg	Asp	Asp	Gly	Thr	Thr	Ala	Ser	Ser	Cys
				725					730					735
Ile	Tyr	Thr	Gly	Ser	Trp	Thr	Glu	Gln	Gly	Asn	Gln	Met	Ala	Asn
			740					745					750	
Asp	Asn	Ser	Asp	Pro	Ser	Gly	Leu	Gly	Asn	Thr	Leu	Gly	Trp	Ala
		755					760					765		
Ala	Trp	Pro	Leu	Asn	Arg	Arg	Val	Leu	Tyr	Asn	Arg	Ala	Ser	Ala
	770					775					780			
Ile	Asn	Gly	Lys	Pro	Trp	Asp	Pro	Lys	Arg	Met	Leu	Ile	Gln	Trp
785					790					795				800
Gly	Ser	Lys	Trp	Thr	Gly	Asn	Asp	Ile	Pro	Asp	Phe	Gly	Asn	Ala
				805					810					815
Pro	Gly	Thr	Pro	Thr	Gly	Pro	Phe	Ile	Met	Gln	Pro	Glu	Gly	Met
			820					825					830	
Arg	Leu	Phe	Ala	Ile	Asn	Lys	Met	Ala	Glu	Gly	Pro	Phe	Pro	Glu
		835					840					845		
Tyr	Glu	Pro	Ile	Glu	Thr	Pro	Leu	Gly	Thr	Asn	Pro	Leu	His	Pro
	850					855					860			
Val	Val	Ser	Asn	Pro	Val	Val	Arg	Leu	Tyr	Glu	Gln	Asp	Ala	Leu
865					870					875				880
Met	Gly	Lys	Lys	Glu	Gln	Phe	Pro	Tyr	Val	Gly	Thr	Thr	Tyr	Arg
				885					890					895
Thr	Glu	His	Phe	His	Thr	Trp	Thr	Lys	His	Ala	Leu	Leu	Asn	Ala
			900					905					910	
Ala	Gln	Pro	Glu	Gln	Phe	Val	Glu	Ile	Ser	Glu	Thr	Leu	Ala	Ala
		915					920					925		
Lys	Gly	Ile	Asn	Asn	Gly	Asp	Arg	Val	Thr	Val	Ser	Ser	Lys	Arg
	930					935					940			
Phe	Ile	Arg	Ala	Val	Ala	Val	Val	Thr	Arg	Arg	Leu	Lys	Pro	Leu
945					950				955					960
Val	Asn	Gly	Gln	Gln	Val	Glu	Thr	Val	Gly	Ile	Pro	Ile	His	Trp
				965					970					975
Phe	Glu	Gly	Val	Ala	Arg	Lys	Gly	Tyr	Ile	Ala	Asn	Thr	Leu	Thr
			980					985					990	
Asn	Val	Gly	Asp	Ala	Asn	Ser	Gln	Thr	Pro	Glu	Tyr	Lys	Ala	Phe
		995					1000					1005		
Val	Asn	Ile	Glu	Lys	Ala									
														1010

<210> 267

<211> 294

<212> PRT

<213> E. Coli

<400> 267

Met	Ala	Met	Glu	Thr	Gln	Asp	Ile	Ile	Lys	Arg	Ser	Ala	Thr	Asn	Ser
1				5					10					15	
Ile	Thr	Pro	Pro	Ser	Gln	Val	Arg	Asp	Tyr	Lys	Ala	Glu	Val	Ala	Lys
			20					25					30		
Leu	Ile	Asp	Val	Ser	Thr	Cys	Ile	Gly	Cys	Lys	Ala	Cys	Gln	Val	Ala
		35					40					45			
Cys	Ser	Glu	Trp	Asn	Asp	Ile	Arg	Asp	Glu	Val	Gly	His	Cys	Val	Gly
	50				55						60				
Val	Tyr	Asp	Asn	Pro	Ala	Asp	Leu	Ser	Ala	Lys	Ser	Trp	Thr	Val	Met
65				70					75					80	
Arg	Phe	Ser	Glu	Thr	Glu	Gln	Asn	Gly	Lys	Leu	Glu	Trp	Leu	Ile	Arg

Lys Gly Ser Ile Lys Gly Met Ile Glu Gly Lys Val Ser Arg Arg Trp
 180 185 190
 Ala Lys Lys His His Pro Arg Trp Tyr Arg Glu Ile Glu Lys Ala Glu
 195 200 205
 Ala Lys Lys Glu Ser Glu Glu Gly Ile
 210 215

<210> 269
 <211> 86
 <212> PRT
 <213> E. Coli

<400> 269
 Met Ala Leu Leu Ile Thr Lys Lys Cys Ile Asn Cys Asp Met Cys Glu
 1 5 10 15
 Pro Glu Cys Pro Asn Glu Ala Ile Ser Met Gly Asp His Ile Tyr Glu
 20 25 30
 Ile Asn Ser Asp Lys Cys Thr Glu Cys Val Gly His Tyr Glu Thr Pro
 35 40 45
 Thr Cys Gln Lys Val Cys Pro Ile Pro Asn Thr Ile Val Lys Asp Pro
 50 55 60
 Ala His Val Glu Thr Glu Glu Gln Leu Trp Asp Lys Phe Val Leu Met
 65 70 75 80
 His His Ala Asp Lys Ile
 85

<210> 270
 <211> 400
 <212> PRT
 <213> E. Coli

<400> 270
 Met Gln Ser Val Asp Val Ala Ile Val Gly Gly Gly Met Val Gly Leu
 1 5 10 15
 Ala Val Ala Cys Gly Leu Gln Gly Ser Gly Leu Arg Val Ala Val Leu
 20 25 30
 Glu Gln Arg Val Gln Glu Pro Leu Ala Ala Asn Ala Pro Pro Gln Leu
 35 40 45
 Arg Val Ser Ala Ile Asn Ala Ala Ser Glu Lys Leu Leu Thr Arg Leu
 50 55 60
 Gly Val Trp Gln Asp Ile Leu Ser Arg Arg Ala Ser Cys Tyr His Gly
 65 70 75 80
 Met Glu Val Trp Asp Lys Asp Ser Phe Gly His Ile Ser Phe Asp Asp
 85 90 95
 Gln Ser Met Gly Tyr Ser His Leu Gly His Ile Val Glu Asn Ser Val
 100 105 110
 Ile His Tyr Ala Leu Trp Asn Lys Ala His Gln Ser Ser Asp Ile Thr
 115 120 125
 Leu Leu Ala Pro Ala Glu Leu Gln Gln Val Ala Trp Gly Glu Asn Glu
 130 135 140
 Thr Phe Leu Thr Leu Lys Asp Gly Ser Met Leu Thr Ala Arg Leu Val
 145 150 155 160
 Ile Gly Ala Asp Gly Ala Asn Ser Trp Leu Arg Asn Lys Ala Asp Ile
 165 170 175
 Pro Leu Thr Phe Trp Asp Tyr Gln His His Ala Leu Val Ala Thr Ile

Gln	Gln	Glu	Pro	Tyr	Glu	Gln	Leu	Ala	Val	Ile	Ala	Asn	Val	Ala	Thr
			180					185					190		
Ser	Val	Ala	His	Glu	Gly	Arg	Ala	Phe	Glu	Arg	Phe	Thr	Gln	His	Gly
		195					200					205			
Pro	Leu	Ala	Met	Leu	Pro	Met	Ser	Asp	Gly	Arg	Cys	Ser	Leu	Val	Trp
	210					215					220				
Cys	His	Pro	Leu	Glu	Arg	Arg	Glu	Glu	Val	Leu	Ser	Trp	Ser	Asp	Glu
225					230					235					240
Lys	Phe	Cys	Arg	Glu	Leu	Gln	Ser	Ala	Phe	Gly	Trp	Arg	Leu	Gly	Lys
				245					250					255	
Ile	Thr	His	Ala	Gly	Lys	Arg	Ser	Ala	Tyr	Pro	Leu	Ala	Leu	Thr	His
			260					265					270		
Ala	Ala	Arg	Ser	Ile	Thr	His	Arg	Thr	Val	Leu	Val	Gly	Asn	Ala	Ala
		275					280					285			
Gln	Thr	Leu	His	Pro	Ile	Ala	Gly	Gln	Gly	Phe	Asn	Leu	Gly	Met	Arg
	290					295					300				
Asp	Val	Met	Ser	Leu	Ala	Glu	Thr	Leu	Thr	Gln	Ala	Gln	Glu	Arg	Gly
305					310					315					320
Glu	Asp	Met	Gly	Asp	Tyr	Gly	Val	Leu	Cys	Arg	Tyr	Gln	Gln	Arg	Arg
			325						330					335	
Gln	Ser	Asp	Arg	Glu	Ala	Thr	Ile	Gly	Val	Thr	Asp	Ser	Leu	Val	His
		340						345					350		
Leu	Phe	Ala	Asn	Arg	Trp	Ala	Pro	Leu	Val	Val	Gly	Arg	Asn	Ile	Gly
	355					360					365				
Leu	Met	Thr	Met	Glu	Leu	Phe	Thr	Pro	Ala	Arg	Asp	Val	Leu	Ala	Gln
	370					375					380				
Arg	Thr	Leu	Gly	Trp	Val	Ala	Arg								
385					390										

<210> 272

<211> 441

<212> PRT

<213> E. Coli

<400> 272

Met	Ser	Glu	Ile	Ser	Arg	Gln	Glu	Phe	Gln	Arg	Arg	Arg	Gln	Ala	Leu
1				5					10					15	
Val	Glu	Gln	Met	Gln	Pro	Gly	Ser	Ala	Ala	Leu	Ile	Phe	Ala	Ala	Pro
			20					25					30		
Glu	Val	Thr	Arg	Ser	Ala	Asp	Ser	Glu	Tyr	Pro	Tyr	Arg	Gln	Asn	Ser
		35					40					45			
Asp	Phe	Trp	Tyr	Phe	Thr	Gly	Phe	Asn	Glu	Pro	Glu	Ala	Val	Leu	Val
	50					55					60				
Leu	Ile	Lys	Ser	Asp	Asp	Thr	His	Asn	His	Ser	Val	Leu	Phe	Asn	Arg
65					70					75					80
Val	Arg	Asp	Leu	Thr	Ala	Glu	Ile	Trp	Phe	Gly	Arg	Arg	Leu	Gly	Gln
				85					90					95	
Asp	Ala	Ala	Pro	Glu	Lys	Leu	Gly	Val	Asp	Arg	Ala	Leu	Ala	Phe	Ser
			100					105					110		
Glu	Ile	Asn	Gln	Gln	Leu	Tyr	Gln	Leu	Leu	Asn	Gly	Leu	Asp	Val	Val
		115					120					125			
Tyr	His	Ala	Gln	Gly	Glu	Tyr	Ala	Tyr	Ala	Asp	Val	Ile	Val	Asn	Ser
	130					135					140				
Ala	Leu	Glu	Lys	Leu	Arg	Lys	Gly	Ser	Arg	Gln	Asn	Leu	Thr	Ala	Pro
145					150					155					160
Ala	Thr	Met	Ile	Asp	Trp	Arg	Pro	Val	Val	His	Glu	Met	Arg	Leu	Phe

				165					170					175
Lys	Ser	Pro	Glu	Ile	Ala	Val	Leu	Arg	Arg	Ala	Gly	Glu	Ile	Thr
			180				185					190		
Ala	Met	Ala	His	Thr	Arg	Ala	Met	Glu	Lys	Cys	Arg	Pro	Gly	Met
		195					200					205		Phe
Glu	Tyr	His	Leu	Glu	Gly	Glu	Ile	His	His	Glu	Phe	Asn	Arg	His
	210					215					220			Gly
Ala	Arg	Tyr	Pro	Ser	Tyr	Asn	Thr	Ile	Val	Gly	Ser	Gly	Glu	Asn
225					230					235				240
Cys	Ile	Leu	His	Tyr	Thr	Glu	Asn	Glu	Cys	Glu	Met	Arg	Asp	Gly
			245						250					255
Leu	Val	Leu	Ile	Asp	Ala	Gly	Cys	Glu	Tyr	Lys	Gly	Tyr	Ala	Gly
		260						265					270	Asp
Ile	Thr	Arg	Thr	Phe	Pro	Val	Asn	Gly	Lys	Phe	Thr	Gln	Ala	Gln
	275						280					285		Arg
Glu	Ile	Tyr	Asp	Ile	Val	Leu	Glu	Ser	Leu	Glu	Thr	Ser	Leu	Arg
	290					295					300			Leu
Tyr	Arg	Pro	Gly	Thr	Ser	Ile	Leu	Glu	Val	Thr	Gly	Glu	Val	Val
305					310					315				Arg
Ile	Met	Val	Ser	Gly	Leu	Val	Lys	Leu	Gly	Ile	Leu	Lys	Gly	Asp
			325						330					Val
Asp	Glu	Leu	Ile	Ala	Gln	Asn	Ala	His	Arg	Pro	Phe	Phe	Met	His
		340						345					350	Gly
Leu	Ser	His	Trp	Leu	Gly	Leu	Asp	Val	His	Asp	Val	Gly	Val	Tyr
	355						360					365		Gly
Gln	Asp	Arg	Ser	Arg	Ile	Leu	Glu	Pro	Gly	Met	Val	Leu	Thr	Val
	370					375					380			Glu
Pro	Gly	Leu	Tyr	Ile	Ala	Pro	Asp	Ala	Glu	Val	Pro	Glu	Gln	Tyr
385					390					395				Arg
Gly	Ile	Gly	Ile	Arg	Ile	Glu	Asp	Asp	Ile	Val	Ile	Thr	Glu	Thr
			405						410					Gly
Asn	Glu	Asn	Leu	Thr	Ala	Ser	Val	Val	Lys	Lys	Pro	Glu	Glu	Ile
		420						425					430	Glu
Ala	Leu	Met	Val	Ala	Ala	Arg	Lys	Gln						
	435						440							

<210> 273
 <211> 194
 <212> PRT
 <213> E. Coli

Met	Leu	Met	Ser	Ile	Gln	Asn	Glu	Met	Pro	Gly	Tyr	Asn	Glu	Met
1				5					10				15	Asn
Gln	Tyr	Leu	Asn	Gln	Gln	Gly	Thr	Gly	Leu	Thr	Pro	Ala	Glu	Met
		20						25					30	His
Gly	Leu	Ile	Ser	Gly	Met	Ile	Cys	Gly	Gly	Asn	Asp	Asp	Ser	Ser
	35					40					45			Trp
Leu	Pro	Leu	Leu	His	Asp	Leu	Thr	Asn	Glu	Gly	Met	Ala	Phe	Gly
	50					55				60				His
Glu	Leu	Ala	Gln	Ala	Leu	Arg	Lys	Met	His	Ser	Ala	Thr	Ser	Asp
65					70					75				Ala
Leu	Gln	Asp	Asp	Gly	Phe	Leu	Phe	Gln	Leu	Tyr	Leu	Pro	Asp	Gly
			85						90				95	Asp
Asp	Val	Ser	Val	Phe	Asp	Arg	Ala	Asp	Ala	Leu	Ala	Gly	Trp	Val
		100						105					110	Asn

His	Phe	Leu	Leu	Gly	Leu	Gly	Val	Thr	Gln	Pro	Lys	Leu	Asp	Lys	Val
	115						120					125			
Thr	Gly	Glu	Thr	Gly	Glu	Ala	Ile	Asp	Asp	Leu	Arg	Asn	Ile	Ala	Gln
	130					135					140				
Leu	Gly	Tyr	Asp	Glu	Asp	Glu	Asp	Gln	Glu	Glu	Leu	Glu	Met	Ser	Leu
145					150					155					160
Glu	Glu	Ile	Ile	Glu	Tyr	Val	Arg	Val	Ala	Ala	Leu	Leu	Cys	His	Asp
				165					170					175	
Thr	Phe	Thr	His	Pro	Gln	Pro	Thr	Ala	Pro	Glu	Val	Gln	Lys	Pro	Thr
			180					185					190		
Leu	His														

<210> 274
 <211> 120
 <212> PRT
 <213> E. Coli

<400> 274

Met	Leu	Lys	Leu	Phe	Ala	Lys	Tyr	Thr	Ser	Ile	Gly	Val	Leu	Asn	Thr
1				5					10					15	
Leu	Ile	His	Trp	Val	Val	Phe	Gly	Val	Cys	Ile	Tyr	Val	Ala	His	Thr
			20					25					30		
Asn	Gln	Ala	Leu	Ala	Asn	Phe	Ala	Gly	Phe	Val	Val	Ala	Val	Ser	Phe
			35				40					45			
Ser	Phe	Phe	Ala	Asn	Ala	Lys	Phe	Thr	Phe	Lys	Ala	Ser	Thr	Thr	Thr
	50					55					60				
Met	Arg	Tyr	Met	Leu	Tyr	Val	Gly	Phe	Met	Gly	Thr	Leu	Ser	Ala	Thr
65					70					75					80
Val	Gly	Trp	Ala	Ala	Asp	Arg	Cys	Ala	Leu	Pro	Pro	Met	Ile	Thr	Leu
				85					90					95	
Val	Thr	Phe	Ser	Ala	Ile	Ser	Leu	Val	Cys	Gly	Phe	Val	Tyr	Ser	Lys
			100					105					110		
Phe	Ile	Val	Phe	Arg	Asp	Ala	Lys								
		115					120								

<210> 275
 <211> 306
 <212> PRT
 <213> E. Coli

<400> 275

Met	Lys	Ile	Ser	Leu	Val	Val	Pro	Val	Phe	Asn	Glu	Glu	Glu	Ala	Ile
1				5					10					15	
Pro	Ile	Phe	Tyr	Lys	Thr	Val	Arg	Glu	Phe	Glu	Glu	Leu	Lys	Ser	Tyr
			20					25					30		
Glu	Val	Glu	Ile	Val	Phe	Ile	Asn	Asp	Gly	Ser	Lys	Asp	Ala	Thr	Glu
			35				40					45			
Ser	Ile	Ile	Asn	Ala	Leu	Ala	Val	Ser	Asp	Pro	Leu	Val	Val	Pro	Leu
			50			55					60				
Ser	Phe	Thr	Arg	Asn	Phe	Gly	Lys	Glu	Pro	Ala	Leu	Phe	Ala	Gly	Leu
65					70					75					80
Asp	His	Ala	Thr	Gly	Asp	Ala	Ile	Ile	Pro	Ile	Asp	Val	Asp	Leu	Gln
				85					90					95	
Asp	Pro	Ile	Glu	Val	Ile	Pro	His	Leu	Ile	Glu	Lys	Trp	Gln	Ala	Gly
			100					105					110		

Ala Asp Met Val Leu Ala Lys Arg Ser Asp Arg Ser Thr Asp Gly Arg
 115 120 125
 Leu Lys Arg Lys Thr Ala Glu Trp Phe Tyr Lys Leu His Asn Lys Ile
 130 135 140
 Ser Asn Pro Lys Ile Glu Asn Val Gly Asp Phe Arg Leu Met Ser
 145 150 155 160
 Arg Asp Val Val Glu Asn Ile Lys Leu Met Pro Glu Arg Asn Leu Phe
 165 170 175
 Met Lys Gly Ile Leu Ser Trp Val Gly Gly Lys Thr Asp Ile Val Glu
 180 185 190
 Tyr Val Arg Ala Glu Arg Ile Ala Gly Asp Thr Lys Phe Asn Gly Trp
 195 200 205
 Lys Leu Trp Asn Leu Ala Leu Glu Gly Ile Thr Ser Phe Ser Thr Phe
 210 215 220
 Pro Leu Arg Ile Trp Thr Tyr Ile Gly Leu Val Val Ala Ser Val Ala
 225 230 235 240
 Phe Ile Tyr Gly Ala Trp Met Ile Leu Asp Thr Ile Ile Phe Gly Asn
 245 250 255
 Ala Val Arg Gly Tyr Pro Ser Leu Leu Val Ser Ile Leu Phe Leu Gly
 260 265 270
 Gly Ile Gln Met Ile Gly Ile Gly Val Leu Gly Glu Tyr Ile Gly Arg
 275 280 285
 Thr Tyr Ile Glu Thr Lys Lys Arg Pro Lys Tyr Ile Ile Lys Arg Val
 290 295 300
 Lys Lys
 305

<210> 276
 <211> 443
 <212> PRT
 <213> E. Coli

<400> 276
 Met Asn Lys Ala Ile Lys Val Ser Leu Tyr Ile Ser Phe Val Leu Ile
 1 5 10 15
 Ile Cys Ala Leu Ser Lys Asn Ile Met Met Leu Asn Thr Ser Asp Phe
 20 25 30
 Gly Arg Ala Ile Lys Pro Leu Ile Glu Asp Ile Pro Ala Phe Thr Tyr
 35 40 45
 Asp Leu Pro Leu Leu Tyr Lys Leu Lys Gly His Ile Asp Ser Ile Asp
 50 55 60
 Ser Tyr Glu Tyr Ile Ser Ser Tyr Ser Tyr Ile Leu Tyr Thr Tyr Val
 65 70 75 80
 Leu Phe Ile Ser Ile Phe Thr Glu Tyr Leu Asp Ala Arg Val Leu Ser
 85 90 95
 Leu Phe Leu Lys Val Ile Tyr Ile Tyr Ser Leu Tyr Ala Ile Phe Thr
 100 105 110
 Ser Tyr Ile Lys Thr Glu Arg Tyr Val Thr Leu Phe Thr Phe Phe Ile
 115 120 125
 Leu Ala Phe Leu Met Cys Ser Ser Ser Thr Leu Ser Met Phe Ala Ser
 130 135 140
 Phe Tyr Gln Glu Gln Ile Val Ile Ile Phe Leu Pro Phe Leu Val Tyr
 145 150 155 160
 Ser Leu Thr Cys Lys Asn Asn Lys Ser Met Leu Leu Leu Phe Phe Ser
 165 170 175
 Leu Leu Ile Ile Ser Thr Ala Lys Asn Gln Phe Ile Leu Thr Pro Leu

<211> 60
 <212> PRT
 <213> E. Coli

<400> 278
 Met Gly Lys Ala Thr Tyr Thr Val Thr Val Thr Asn Asn Ser Asn Gly
 1 5 10 15
 Val Ser Val Asp Tyr Glu Thr Glu Thr Pro Met Thr Leu Leu Val Pro
 20 25 30
 Glu Val Ala Ala Glu Val Ile Lys Asp Leu Val Asn Thr Val Arg Ser
 35 40 45
 Tyr Asp Thr Glu Asn Glu His Asp Val Cys Gly Trp
 50 55 60

<210> 279
 <211> 119
 <212> PRT
 <213> E. Coli

<400> 279
 Met Leu Gln Ile Pro Gln Asn Tyr Ile His Thr Arg Ser Thr Pro Phe
 1 5 10 15
 Trp Asn Lys Gln Thr Ala Pro Ala Gly Ile Phe Glu Arg His Leu Asp
 20 25 30
 Lys Gly Thr Arg Pro Gly Val Tyr Pro Arg Leu Ser Val Met His Gly
 35 40 45
 Ala Val Lys Tyr Leu Gly Tyr Ala Asp Glu His Ser Ala Glu Pro Asp
 50 55 60
 Gln Val Ile Leu Ile Glu Ala Gly Gln Phe Ala Val Phe Pro Pro Glu
 65 70 75 80
 Lys Trp His Asn Ile Glu Ala Met Thr Asp Asp Thr Tyr Phe Asn Ile
 85 90 95
 Asp Phe Phe Val Ala Pro Glu Val Leu Met Glu Gly Ala Gln Gln Arg
 100 105 110
 Lys Val Ile His Asn Gly Lys
 115

<210> 280
 <211> 246
 <212> PRT
 <213> E. Coli

<400> 280
 Met Lys Phe Lys Val Ile Ala Leu Ala Ala Leu Met Gly Ile Ser Gly
 1 5 10 15
 Met Ala Ala Gln Ala Asn Glu Leu Pro Asp Gly Pro His Ile Val Thr
 20 25 30
 Ser Gly Thr Ala Ser Val Asp Ala Val Pro Asp Ile Ala Thr Leu Ala
 35 40 45
 Ile Glu Val Asn Val Ala Ala Lys Asp Ala Ala Thr Ala Lys Lys Gln
 50 55 60
 Ala Asp Glu Arg Val Ala Gln Tyr Ile Ser Phe Leu Glu Leu Asn Gln
 65 70 75 80
 Ile Ala Lys Lys Asp Ile Ser Ser Ala Asn Leu Arg Thr Gln Pro Asp
 85 90 95

Tyr	Asp	Tyr	Gln	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Gly	Tyr	Arg	Ala	Val
			100					105					110		
Arg	Thr	Val	Glu	Val	Thr	Leu	Arg	Gln	Leu	Asp	Lys	Leu	Asn	Ser	Leu
		115					120					125			
Leu	Asp	Gly	Ala	Leu	Lys	Ala	Gly	Leu	Asn	Glu	Ile	Arg	Ser	Val	Ser
	130					135					140				
Leu	Gly	Val	Ala	Gln	Pro	Asp	Ala	Tyr	Lys	Asp	Lys	Ala	Arg	Lys	Ala
145					150					155					160
Ala	Ile	Asp	Asn	Ala	Ile	His	Gln	Ala	Gln	Glu	Leu	Ala	Asn	Gly	Phe
			165						170					175	
His	Arg	Lys	Leu	Gly	Pro	Val	Tyr	Ser	Val	Arg	Tyr	His	Val	Ser	Asn
		180						185					190		
Tyr	Gln	Pro	Ser	Pro	Met	Val	Arg	Met	Met	Lys	Ala	Asp	Ala	Ala	Pro
		195					200					205			
Val	Ser	Ala	Gln	Glu	Thr	Tyr	Glu	Gln	Ala	Ala	Ile	Gln	Phe	Asp	Asp
	210					215					220				
Gln	Val	Asp	Val	Val	Phe	Gln	Leu	Glu	Pro	Val	Asp	Gln	Gln	Pro	Ala
225					230					235					240
Lys	Thr	Pro	Ala	Ala	Gln										
				245											

<210> 281

<211> 464

<212> PRT

<213> E. Coli

<400> 281

Met	Leu	Leu	Leu	Asp	Ala	Cys	Ser	Gln	Met	Cys	Pro	Ser	Phe	Arg	Arg
1				5					10					15	
Phe	Gln	Thr	Val	Phe	His	Asn	Ser	Ser	Ile	Phe	Leu	Pro	Tyr	Trp	Leu
			20					25					30		
Ala	Thr	Leu	Val	Ser	Phe	Arg	Glu	Thr	Phe	Gln	Glu	Glu	Lys	Leu	Leu
		35					40					45			
Thr	Met	Lys	Gly	Ser	Tyr	Lys	Ser	Arg	Trp	Val	Ile	Val	Ile	Val	Val
	50					55					60				
Val	Ile	Ala	Ala	Ile	Ala	Ala	Phe	Trp	Phe	Trp	Gln	Gly	Arg	Asn	Asp
65				70					75					80	
Ser	Arg	Ser	Ala	Ala	Pro	Gly	Ala	Thr	Lys	Gln	Ala	Gln	Gln	Ser	Pro
			85						90					95	
Ala	Gly	Gly	Arg	Arg	Gly	Met	Arg	Ser	Gly	Pro	Leu	Ala	Pro	Val	Gln
		100						105					110		
Ala	Ala	Thr	Ala	Val	Glu	Gln	Ala	Val	Pro	Arg	Tyr	Leu	Thr	Gly	Leu
		115					120					125			
Gly	Thr	Ile	Thr	Ala	Ala	Asn	Thr	Val	Thr	Val	Arg	Ser	Arg	Val	Asp
	130					135					140				
Gly	Gln	Leu	Ile	Ala	Leu	His	Phe	Gln	Glu	Gly	Gln	Gln	Val	Lys	Ala
145					150					155					160
Gly	Asp	Leu	Leu	Ala	Glu	Ile	Asp	Pro	Ser	Gln	Phe	Lys	Val	Ala	Leu
				165					170					175	
Ala	Gln	Ala	Gln	Gly	Gln	Leu	Ala	Lys	Asp	Lys	Ala	Thr	Leu	Ala	Asn
			180					185					190		
Ala	Arg	Arg	Asp	Leu	Ala	Arg	Tyr	Gln	Gln	Leu	Ala	Lys	Thr	Asn	Leu
	195						200					205			
Val	Ser	Arg	Gln	Glu	Leu	Asp	Ala	Gln	Gln	Ala	Leu	Val	Ser	Glu	Thr
	210					215					220				
Glu	Gly	Thr	Ile	Lys	Ala	Asp	Glu	Ala	Ser	Val	Ala	Ser	Ala	Gln	Leu

225		230		235		240									
Gln	Leu	Asp	Trp	Ser	Arg	Ile	Thr	Ala	Pro	Val	Asp	Gly	Arg	Val	Gly
		245							250					255	
Leu	Lys	Gln	Val	Asp	Val	Gly	Asn	Gln	Ile	Ser	Ser	Gly	Asp	Thr	Thr
		260						265					270		
Gly	Ile	Val	Val	Ile	Thr	Gln	Thr	His	Pro	Ile	Asp	Leu	Val	Phe	Thr
		275					280					285			
Leu	Pro	Glu	Ser	Asp	Ile	Ala	Thr	Val	Val	Gln	Ala	Gln	Lys	Ala	Gly
	290					295				300					
Lys	Pro	Leu	Val	Val	Glu	Ala	Trp	Asp	Arg	Thr	Asn	Ser	Lys	Lys	Leu
305					310					315					320
Ser	Glu	Gly	Thr	Leu	Leu	Ser	Leu	Asp	Asn	Gln	Ile	Asp	Ala	Thr	Thr
				325				330						335	
Gly	Thr	Ile	Lys	Val	Lys	Ala	Arg	Phe	Asn	Asn	Gln	Asp	Asp	Ala	Leu
		340				345							350		
Phe	Pro	Asn	Gln	Phe	Val	Asn	Ala	Arg	Met	Leu	Val	Asp	Thr	Glu	Gln
		355				360						365			
Asn	Ala	Val	Val	Ile	Pro	Thr	Ala	Ala	Leu	Gln	Met	Gly	Asn	Glu	Gly
	370					375					380				
His	Phe	Val	Trp	Val	Leu	Asn	Ser	Glu	Asn	Lys	Val	Ser	Lys	His	Leu
385					390					395					400
Val	Thr	Pro	Gly	Ile	Gln	Asp	Ser	Gln	Lys	Val	Val	Ile	Arg	Ala	Gly
			405					410					415		
Ile	Ser	Ala	Gly	Asp	Arg	Val	Val	Thr	Asp	Gly	Ile	Asp	Arg	Leu	Thr
			420					425					430		
Glu	Gly	Ala	Lys	Val	Glu	Val	Val	Glu	Ala	Gln	Ser	Ala	Thr	Thr	Pro
		435				440					445				
Glu	Glu	Lys	Ala	Thr	Ser	Arg	Glu	Tyr	Ala	Lys	Lys	Gly	Ala	Arg	Ser
	450					455					460				

<210> 282
 <211> 1040
 <212> PRT
 <213> E. Coli

<400> 282

Met	Gln	Val	Leu	Pro	Pro	Ser	Ser	Thr	Gly	Gly	Pro	Ser	Arg	Leu	Phe
1				5					10					15	
Ile	Met	Arg	Pro	Val	Ala	Thr	Thr	Leu	Leu	Met	Val	Ala	Ile	Leu	Leu
			20					25					30		
Ala	Gly	Ile	Ile	Gly	Tyr	Arg	Ala	Leu	Pro	Val	Ser	Ala	Leu	Pro	Glu
		35					40					45			
Val	Asp	Tyr	Pro	Thr	Ile	Gln	Val	Val	Thr	Leu	Tyr	Pro	Gly	Ala	Ser
	50					55					60				
Pro	Asp	Val	Met	Thr	Ser	Ala	Val	Thr	Ala	Pro	Leu	Glu	Arg	Gln	Phe
65					70					75					80
Gly	Gln	Met	Ser	Gly	Leu	Lys	Gln	Met	Ser	Ser	Gln	Ser	Ser	Gly	Gly
			85					90						95	
Ala	Ser	Val	Ile	Thr	Leu	Gln	Phe	Gln	Leu	Thr	Leu	Pro	Leu	Asp	Val
			100					105					110		
Ala	Glu	Gln	Glu	Val	Gln	Ala	Ala	Ile	Asn	Ala	Ala	Thr	Asn	Leu	Leu
		115				120						125			
Pro	Ser	Asp	Leu	Pro	Asn	Pro	Pro	Val	Tyr	Ser	Lys	Val	Asn	Pro	Ala
	130				135					140					
Asp	Pro	Pro	Ile	Met	Thr	Leu	Ala	Val	Thr	Ser	Thr	Ala	Met	Pro	Met
145					150					155					160

Thr	Gln	Val	Glu	Asp	Met	Val	Glu	Thr	Arg	Val	Ala	Gln	Lys	Ile	Ser	165	170	175
Gln	Ile	Ser	Gly	Val	Gly	Leu	Val	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Pro	180	185	190
Ala	Val	Arg	Val	Lys	Leu	Asn	Ala	Gln	Ala	Ile	Ala	Ala	Leu	Gly	Leu	195	200	205
Thr	Ser	Glu	Thr	Val	Arg	Thr	Ala	Ile	Thr	Gly	Ala	Asn	Val	Asn	Ser	210	215	220
Ala	Lys	Gly	Ser	Leu	Asp	Gly	Pro	Ser	Arg	Ala	Val	Thr	Leu	Ser	Ala	225	230	235
Asn	Asp	Gln	Met	Gln	Ser	Ala	Glu	Glu	Tyr	Arg	Gln	Leu	Ile	Ile	Ala	245	250	255
Tyr	Gln	Asn	Gly	Ala	Pro	Ile	Arg	Leu	Gly	Asp	Val	Ala	Thr	Val	Glu	260	265	270
Gln	Gly	Ala	Glu	Asn	Ser	Trp	Leu	Gly	Ala	Trp	Ala	Asn	Lys	Glu	Gln	275	280	285
Ala	Ile	Val	Met	Asn	Val	Gln	Arg	Gln	Pro	Gly	Ala	Asn	Ile	Ile	Ser	290	295	300
Thr	Ala	Asp	Ser	Ile	Arg	Gln	Met	Leu	Pro	Gln	Leu	Thr	Glu	Ser	Leu	305	310	315
Pro	Lys	Ser	Val	Lys	Val	Thr	Val	Leu	Ser	Asp	Arg	Thr	Thr	Asn	Ile	325	330	335
Arg	Ala	Ser	Val	Asp	Asp	Thr	Gln	Phe	Glu	Leu	Met	Met	Ala	Ile	Ala	340	345	350
Leu	Val	Val	Met	Ile	Ile	Tyr	Leu	Phe	Leu	Arg	Asn	Ile	Pro	Ala	Thr	355	360	365
Ile	Ile	Pro	Gly	Val	Ala	Val	Pro	Leu	Ser	Leu	Ile	Gly	Thr	Phe	Ala	370	375	380
Val	Met	Val	Phe	Leu	Asp	Phe	Ser	Ile	Asn	Asn	Leu	Thr	Leu	Met	Ala	385	390	395
Leu	Thr	Ile	Ala	Thr	Gly	Phe	Val	Val	Asp	Asp	Ala	Ile	Val	Val	Ile	405	410	415
Glu	Asn	Ile	Ser	Arg	Tyr	Ile	Glu	Lys	Gly	Glu	Lys	Pro	Leu	Ala	Ala	420	425	430
Ala	Leu	Lys	Gly	Ala	Gly	Glu	Ile	Gly	Phe	Thr	Ile	Ile	Ser	Leu	Thr	435	440	445
Phe	Ser	Leu	Ile	Ala	Val	Leu	Ile	Pro	Leu	Leu	Phe	Met	Gly	Asp	Ile	450	455	460
Val	Gly	Arg	Leu	Phe	Arg	Glu	Phe	Ala	Ile	Thr	Leu	Ala	Val	Ala	Ile	465	470	475
Leu	Ile	Ser	Ala	Val	Ser	Leu	Thr	Leu	Thr	Pro	Met	Met	Cys	Ala		485	490	495
Arg	Met	Leu	Ser	Gln	Glu	Ser	Leu	Arg	Lys	Gln	Asn	Arg	Phe	Ser	Arg	500	505	510
Ala	Ser	Glu	Lys	Met	Phe	Asp	Arg	Ile	Ile	Ala	Ala	Tyr	Gly	Arg	Gly	515	520	525
Leu	Ala	Lys	Val	Leu	Asn	His	Pro	Trp	Leu	Thr	Leu	Ser	Val	Ala	Leu	530	535	540
Ser	Thr	Leu	Leu	Leu	Ser	Val	Leu	Leu	Trp	Val	Phe	Ile	Pro	Lys	Gly	545	550	555
Phe	Phe	Pro	Val	Gln	Asp	Asn	Gly	Ile	Ile	Gln	Gly	Thr	Leu	Gln	Ala	565	570	575
Pro	Gln	Ser	Ser	Ser	Phe	Ala	Asn	Met	Ala	Gln	Arg	Gln	Arg	Gln	Val	580	585	590
Ala	Asp	Val	Ile	Leu	Gln	Asp	Pro	Ala	Val	Gln	Ser	Leu	Thr	Ser	Phe	595	600	605
Val	Gly	Val	Asp	Gly	Thr	Asn	Pro	Ser	Leu	Asn	Ser	Ala	Arg	Leu	Gln			

610	615	620
Ile Asn Leu Lys Pro Leu Asp Glu Arg Asp Asp Arg Val Gln Lys Val		
625	630	635
Ile Ala Arg Leu Gln Thr Ala Val Asp Lys Val Pro Gly Val Asp Leu		640
	645	650
Phe Leu Gln Pro Thr Gln Asp Leu Thr Ile Asp Thr Gln Val Ser Arg		655
	660	665
Thr Gln Tyr Gln Phe Thr Leu Gln Ala Thr Ser Leu Asp Ala Leu Ser		670
	675	680
Thr Trp Val Pro Gln Leu Met Glu Lys Leu Gln Gln Leu Pro Gln Leu		685
	690	695
Ser Asp Val Ser Ser Asp Trp Gln Asp Lys Gly Leu Val Ala Tyr Val		700
705	710	715
Asn Val Asp Arg Asp Ser Ala Ser Arg Leu Gly Ile Ser Met Ala Asp		720
	725	730
Val Asp Asn Ala Leu Tyr Asn Ala Phe Gly Gln Arg Leu Ile Ser Thr		735
	740	745
Ile Tyr Thr Gln Ala Asn Gln Tyr Arg Val Val Leu Glu His Asn Thr		750
	755	760
Glu Asn Thr Pro Gly Leu Ala Ala Leu Asp Thr Ile Arg Leu Thr Ser		765
	770	775
Ser Asp Gly Gly Val Val Pro Leu Ser Ser Ile Ala Lys Ile Glu Gln		780
785	790	795
Arg Phe Ala Pro Leu Ser Ile Asn His Leu Asp Gln Phe Pro Val Thr		800
	805	810
Thr Ile Ser Phe Asn Val Pro Asp Asn Tyr Ser Leu Gly Asp Ala Val		815
	820	825
Gln Ala Ile Met Asp Thr Glu Lys Thr Leu Asn Leu Pro Val Asp Ile		830
	835	840
Thr Thr Gln Phe Gln Gly Ser Thr Leu Ala Phe Gln Ser Ala Leu Gly		845
	850	855
Ser Thr Val Trp Leu Ile Val Ala Ala Val Val Ala Met Tyr Ile Val		860
865	870	875
Leu Gly Ile Leu Tyr Glu Ser Phe Ile His Pro Ile Thr Ile Leu Ser		880
	885	890
Thr Leu Pro Thr Ala Gly Val Gly Ala Leu Leu Ala Leu Leu Ile Ala		895
	900	905
Gly Ser Glu Leu Asp Val Ile Ala Ile Ile Gly Ile Ile Leu Leu Ile		910
	915	920
Gly Ile Val Lys Lys Asn Ala Ile Met Met Ile Asp Phe Ala Leu Ala		925
	930	935
Ala Glu Arg Glu Gln Gly Met Ser Pro Arg Glu Ala Ile Tyr Gln Ala		940
945	950	955
Cys Leu Leu Arg Phe Arg Pro Ile Leu Met Thr Thr Leu Ala Ala Leu		960
	965	970
Leu Gly Ala Leu Pro Leu Met Leu Ser Thr Gly Val Gly Ala Glu Leu		975
	980	985
Arg Arg Pro Leu Gly Ile Gly Met Val Gly Gly Leu Ile Val Ser Gln		990
	995	1000
Val Leu Thr Leu Phe Thr Thr Pro Val Ile Tyr Leu Leu Phe Asp Arg		1005
	1010	1015
Leu Ala Leu Trp Thr Lys Ser Arg Phe Ala Arg His Glu Glu Glu Ala		1020
1025	1030	1035
		1040

<210> 283
<211> 1025

<212> PRT
 <213> E. Coli

<400> 283
 Met Lys Phe Phe Ala Leu Phe Ile Tyr Arg Pro Val Ala Thr Ile Leu
 1 5 10 15
 Leu Ser Val Ala Ile Thr Leu Cys Gly Ile Leu Gly Phe Arg Met Leu
 20 25 30
 Pro Val Ala Pro Leu Pro Gln Val Asp Phe Pro Val Ile Ile Val Ser
 35 40 45
 Ala Ser Leu Pro Gly Ala Ser Pro Glu Thr Met Ala Ser Ser Val Ala
 50 55 60
 Thr Pro Leu Glu Arg Ser Leu Gly Arg Ile Ala Gly Val Ser Glu Met
 65 70 75 80
 Thr Ser Ser Ser Ser Leu Gly Ser Thr Arg Ile Ile Leu Gln Phe Asp
 85 90 95
 Phe Asp Arg Asp Ile Asn Gly Ala Ala Arg Asp Val Gln Ala Ala Ile
 100 105 110
 Asn Ala Ala Gln Ser Leu Leu Pro Ser Gly Met Pro Ser Arg Pro Thr
 115 120 125
 Tyr Arg Lys Ala Asn Pro Ser Asp Ala Pro Ile Met Ile Leu Thr Leu
 130 135 140
 Thr Ser Asp Thr Tyr Ser Gln Gly Glu Leu Tyr Asp Phe Ala Ser Thr
 145 150 155 160
 Gln Leu Ala Pro Thr Ile Ser Gln Ile Asp Gly Val Gly Asp Val Asp
 165 170 175
 Val Gly Gly Ser Ser Leu Pro Ala Val Arg Val Gly Leu Asn Pro Gln
 180 185 190
 Ala Leu Phe Asn Gln Gly Val Ser Leu Asp Asp Val Arg Thr Ala Val
 195 200 205
 Ser Asn Ala Asn Val Arg Lys Pro Gln Gly Ala Leu Glu Asp Gly Thr
 210 215 220
 His Arg Trp Gln Ile Gln Thr Asn Asp Glu Leu Lys Thr Ala Ala Glu
 225 230 235 240
 Tyr Gln Pro Leu Ile Ile His Tyr Asn Asn Gly Gly Ala Val Arg Leu
 245 250 255
 Gly Asp Val Ala Thr Val Thr Asp Ser Val Gln Asp Val Arg Asn Ala
 260 265 270
 Gly Met Thr Asn Ala Lys Pro Ala Ile Leu Leu Met Ile Arg Lys Leu
 275 280 285
 Pro Glu Ala Asn Ile Ile Gln Thr Val Asp Ser Ile Arg Ala Lys Leu
 290 295 300
 Pro Glu Leu Gln Glu Thr Ile Pro Ala Ala Ile Asp Leu Gln Ile Ala
 305 310 315 320
 Gln Asp Arg Ser Pro Thr Ile Arg Ala Ser Leu Glu Glu Val Glu Gln
 325 330 335
 Thr Leu Ile Ile Ser Val Ala Leu Val Ile Leu Val Val Phe Leu Phe
 340 345 350
 Leu Arg Ser Gly Arg Ala Thr Ile Ile Pro Ala Val Ser Val Pro Val
 355 360 365
 Ser Leu Ile Gly Thr Phe Ala Ala Met Tyr Leu Cys Gly Phe Ser Leu
 370 375 380
 Asn Asn Leu Ser Leu Met Ala Leu Thr Ile Ala Thr Gly Phe Val Val
 385 390 395 400
 Asp Asp Ala Ile Val Val Leu Glu Asn Ile Ala Arg His Leu Glu Ala
 405 410 415
 Gly Met Lys Pro Leu Gln Ala Ala Leu Gln Gly Thr Arg Glu Val Gly

Leu Ser Thr Leu Pro Ser Ala Gly Val Gly Ala Leu Leu Ala Leu Glu
 885 890 895
 Leu Phe Asn Ala Pro Phe Ser Leu Ile Ala Leu Ile Gly Ile Met Leu
 900 905 910
 Leu Ile Gly Ile Val Lys Lys Asn Ala Ile Met Met Val Asp Phe Ala
 915 920 925
 Leu Glu Ala Gln Arg His Gly Asn Leu Thr Pro Gln Glu Ala Ile Phe
 930 935 940
 Gln Ala Cys Leu Leu Arg Phe Arg Pro Ile Met Met Thr Thr Leu Ala
 945 950 955 960
 Ala Leu Phe Gly Ala Leu Pro Leu Val Leu Ser Gly Gly Asp Gly Ser
 965 970 975
 Glu Leu Arg Gln Pro Leu Gly Ile Thr Ile Val Gly Gly Leu Val Met
 980 985 990
 Ser Gln Leu Leu Thr Leu Tyr Thr Thr Pro Val Val Tyr Leu Phe Phe
 995 1000 1005
 Asp Arg Leu Arg Leu Arg Phe Ser Arg Lys Pro Lys Gln Thr Val Thr
 1010 1015 1020
 Glu
 1025

<210> 284

<211> 471

<212> PRT

<213> E. Coli

<400> 284

Met Thr Asp Leu Pro Asp Ser Thr Arg Trp Gln Leu Trp Ile Val Ala
 1 5 10 15
 Phe Gly Phe Phe Met Gln Ser Leu Asp Thr Thr Ile Val Asn Thr Ala
 20 25 30
 Leu Pro Ser Met Ala Gln Ser Leu Gly Glu Ser Pro Leu His Met His
 35 40 45
 Met Val Ile Val Ser Tyr Val Leu Thr Val Ala Val Met Leu Pro Ala
 50 55 60
 Ser Gly Trp Leu Ala Asp Lys Val Gly Val Arg Asn Ile Phe Phe Thr
 65 70 75 80
 Ala Ile Val Leu Phe Thr Leu Gly Ser Leu Phe Cys Ala Leu Ser Gly
 85 90 95
 Thr Leu Asn Glu Leu Leu Leu Ala Arg Ala Leu Gln Gly Val Gly Gly
 100 105 110
 Ala Met Met Val Pro Val Gly Arg Leu Thr Val Met Lys Ile Val Pro
 115 120 125
 Arg Glu Gln Tyr Met Ala Ala Met Thr Phe Val Thr Leu Pro Gly Gln
 130 135 140
 Val Gly Pro Leu Leu Gly Pro Ala Leu Gly Gly Leu Leu Val Glu Tyr
 145 150 155 160
 Ala Ser Trp His Trp Ile Phe Leu Ile Asn Ile Pro Val Gly Ile Ile
 165 170 175
 Gly Ala Ile Ala Thr Leu Leu Leu Met Pro Asn Tyr Thr Met Gln Thr
 180 185 190
 Arg Arg Phe Asp Leu Ser Gly Phe Leu Leu Leu Ala Val Gly Met Ala
 195 200 205
 Val Leu Thr Leu Ala Leu Asp Gly Ser Lys Gly Thr Gly Leu Ser Pro
 210 215 220
 Leu Thr Ile Ala Gly Leu Val Ala Val Gly Val Val Ala Leu Val Leu

225					230					235				240
Tyr	Leu	Leu	His	Ala	Arg	Asn	Asn	Asn	Arg	Ala	Leu	Phe	Ser	Leu
				245					250					255
Leu	Phe	Arg	Thr	Arg	Thr	Phe	Ser	Leu	Gly	Leu	Ala	Gly	Ser	Phe
			260					265					270	
Gly	Arg	Ile	Gly	Ser	Gly	Met	Leu	Pro	Phe	Met	Thr	Pro	Val	Phe
		275					280					285		
Gln	Ile	Gly	Leu	Gly	Phe	Ser	Pro	Phe	His	Ala	Gly	Leu	Met	Met
	290					295					300			
Pro	Met	Val	Leu	Gly	Ser	Met	Gly	Met	Lys	Arg	Ile	Val	Val	Gln
305					310					315				320
Val	Asn	Arg	Phe	Gly	Tyr	Arg	Arg	Val	Leu	Val	Ala	Thr	Thr	Leu
				325					330					335
Leu	Ser	Leu	Val	Thr	Leu	Leu	Phe	Met	Thr	Thr	Ala	Leu	Leu	Gly
			340					345					350	
Tyr	Tyr	Val	Leu	Pro	Phe	Val	Leu	Phe	Leu	Gln	Gly	Met	Val	Asn
		355					360					365		Ser
Thr	Arg	Phe	Ser	Ser	Met	Asn	Thr	Leu	Thr	Leu	Lys	Asp	Leu	Pro
	370					375					380			Asp
Asn	Leu	Ala	Ser	Ser	Gly	Asn	Ser	Leu	Leu	Ser	Met	Ile	Met	Gln
385					390					395				400
Ser	Met	Ser	Ile	Gly	Val	Thr	Ile	Ala	Gly	Leu	Leu	Leu	Gly	Leu
			405						410					415
Gly	Ser	Gln	His	Val	Ser	Val	Asp	Ser	Gly	Thr	Thr	Gln	Thr	Val
		420						425					430	Phe
Met	Tyr	Thr	Trp	Leu	Ser	Met	Ala	Leu	Ile	Ile	Ala	Leu	Pro	Ala
		435					440					445		Phe
Ile	Phe	Ala	Arg	Val	Pro	Asn	Asp	Thr	His	Gln	Asn	Val	Ala	Ile
	450					455					460			Ser
Arg	Arg	Lys	Arg	Ser	Ala	Gln								
465					470									

<210> 285
 <211> 344
 <212> PRT
 <213> E. Coli

<400> 285

Met	Glu	Ile	Arg	Ile	Met	Leu	Phe	Ile	Leu	Met	Met	Met	Val	Met	Pro
1				5					10					15	
Val	Ser	Tyr	Ala	Ala	Cys	Tyr	Ser	Glu	Leu	Ser	Val	Gln	His	Asn	Leu
			20					25					30		
Val	Val	Gln	Gly	Asp	Phe	Ala	Leu	Thr	Gln	Thr	Gln	Met	Ala	Thr	Tyr
		35					40					45			
Glu	His	Asn	Phe	Asn	Asp	Ser	Ser	Cys	Val	Ser	Thr	Asn	Thr	Ile	Thr
	50				55					60					
Pro	Met	Ser	Pro	Ser	Asp	Ile	Ile	Val	Gly	Leu	Tyr	Asn	Asp	Thr	Ile
65					70				75					80	
Lys	Leu	Asn	Leu	His	Phe	Glu	Trp	Thr	Asn	Lys	Asn	Asn	Ile	Thr	Leu
			85					90					95		
Ser	Asn	Asn	Gln	Thr	Ser	Phe	Thr	Ser	Gly	Tyr	Ser	Val	Thr	Val	Thr
			100				105					110			
Pro	Ala	Ala	Ser	Asn	Ala	Lys	Val	Asn	Val	Ser	Ala	Gly	Gly	Gly	Gly
	115					120						125			
Ser	Val	Met	Ile	Asn	Gly	Val	Ala	Thr	Leu	Ser	Ser	Ala	Ser	Ser	Ser
130						135					140				

Thr Arg Gly Ser Ala Ala Val Gln Phe Leu Leu Cys Leu Leu Gly Gly
 145 150 155 160
 Lys Ser Trp Asp Ala Cys Val Asn Ser Tyr Arg Asn Ala Leu Ala Gln
 165 170 175
 Asn Ala Gly Val Tyr Ser Phe Asn Leu Thr Leu Ser Tyr Asn Pro Ile
 180 185 190
 Thr Thr Thr Cys Lys Pro Asp Asp Leu Leu Ile Thr Leu Asp Ser Ile
 195 200 205
 Pro Val Ser Gln Leu Pro Ala Thr Gly Asn Lys Ala Thr Ile Asn Ser
 210 215 220
 Lys Gln Gly Asp Ile Ile Leu Arg Cys Lys Asn Leu Leu Gly Gln Gln
 225 230 235 240
 Asn Gln Thr Ser Arg Lys Met Gln Val Tyr Leu Ser Ser Ser Asp Leu
 245 250 255
 Leu Thr Asn Ser Asn Thr Ile Leu Lys Gly Ala Glu Asp Asn Gly Val
 260 265 270
 Gly Phe Ile Leu Glu Ser Asn Gly Ser Pro Val Thr Leu Leu Asn Ile
 275 280 285
 Thr Asn Ser Ser Lys Gly Tyr Thr Asn Leu Lys Glu Val Ala Ala Lys
 290 295 300
 Ser Lys Leu Thr Asp Thr Thr Val Ser Ile Pro Ile Thr Ala Ser Tyr
 305 310 315 320
 Tyr Val Tyr Asp Thr Asn Lys Val Lys Ser Gly Ala Leu Glu Ala Thr
 325 330 335
 Ala Leu Ile Asn Val Lys Tyr Asp
 340

<210> 286
 <211> 826
 <212> PRT
 <213> E. Coli

<400> 286
 Met Leu Arg Met Thr Pro Leu Ala Ser Ala Ile Val Ala Leu Leu Leu
 1 5 10 15
 Gly Ile Glu Ala Tyr Ala Ala Glu Glu Thr Phe Asp Thr His Phe Met
 20 25 30
 Ile Gly Gly Met Lys Asp Gln Gln Val Ala Asn Ile Arg Leu Asp Asp
 35 40 45
 Asn Gln Pro Leu Pro Gly Gln Tyr Asp Ile Asp Ile Tyr Val Asn Lys
 50 55 60
 Gln Trp Arg Gly Lys Tyr Glu Ile Ile Val Lys Asp Asn Pro Gln Glu
 65 70 75 80
 Thr Cys Leu Ser Arg Glu Val Ile Lys Arg Leu Gly Ile Asn Ser Asp
 85 90 95
 Asn Phe Ala Ser Gly Lys Gln Cys Leu Thr Phe Glu Gln Leu Val Gln
 100 105 110
 Gly Gly Ser Tyr Thr Trp Asp Ile Gly Val Phe Arg Leu Asp Phe Ser
 115 120 125
 Val Pro Gln Ala Trp Val Glu Glu Leu Glu Ser Gly Tyr Val Pro Pro
 130 135 140
 Glu Asn Trp Glu Arg Gly Ile Asn Ala Phe Tyr Thr Ser Tyr Tyr Leu
 145 150 155 160
 Ser Gln Tyr Tyr Ser Asp Tyr Lys Ala Ser Gly Asn Asn Lys Ser Thr
 165 170 175
 Tyr Val Arg Phe Asn Ser Gly Leu Asn Leu Leu Gly Trp Gln Leu His

Ser Thr Tyr Arg Gln Ala Gly Ala Ser Val Ser Gly Gly Ile Val Ala
 645 650 655
 Trp Ser Gly Gly Val Asn Leu Ala Asn Arg Leu Ser Glu Thr Phe Ala
 660 665 670
 Val Met Asn Ala Pro Gly Ile Lys Asp Ala Tyr Val Asn Gly Gln Lys
 675 680 685
 Tyr Arg Thr Thr Asn Arg Asn Gly Val Val Ile Tyr Asp Gly Met Thr
 690 695 700
 Pro Tyr Arg Glu Asn His Leu Met Leu Asp Val Ser Gln Ser Asp Ser
 705 710 715 720
 Glu Ala Glu Leu Arg Gly Asn Arg Lys Ile Ala Ala Pro Tyr Arg Gly
 725 730 735
 Ala Val Val Leu Val Asn Phe Asp Thr Asp Gln Arg Lys Pro Trp Phe
 740 745 750
 Ile Lys Ala Leu Arg Ala Asp Gly Gln Ser Leu Thr Phe Gly Tyr Glu
 755 760 765
 Val Asn Asp Ile His Gly His Asn Ile Gly Val Val Gly Gln Gly Ser
 770 775 780
 Gln Leu Phe Ile Arg Thr Asn Glu Val Pro Pro Ser Val Asn Val Ala
 785 790 795 800
 Ile Asp Lys Gln Gln Gly Leu Ser Cys Thr Ile Thr Phe Gly Lys Glu
 805 810 815
 Ile Asp Glu Ser Arg Asn Tyr Ile Cys Gln
 820 825

<210> 287

<211> 239

<212> PRT

<213> E. Coli

<400> 287

Met Ala Ala Ile Pro Trp Arg Pro Phe Asn Leu Arg Gly Ile Lys Met
 1 5 10 15
 Lys Gly Leu Leu Ser Leu Leu Ile Phe Ser Met Val Leu Pro Ala His
 20 25 30
 Ala Gly Ile Val Ile Tyr Gly Thr Arg Ile Ile Tyr Pro Ala Glu Asn
 35 40 45
 Lys Glu Val Met Val Gln Leu Met Asn Gln Gly Asn Arg Ser Ser Leu
 50 55 60
 Leu Gln Ala Trp Ile Asp Asp Gly Asp Thr Ser Leu Pro Pro Glu Lys
 65 70 75 80
 Ile Gln Val Pro Phe Met Leu Thr Pro Pro Val Ala Lys Ile Gly Ala
 85 90 95
 Asn Ser Gly Gln Gln Val Lys Ile Lys Ile Met Pro Asn Lys Leu Pro
 100 105 110
 Thr Asn Lys Glu Ser Ile Phe Tyr Leu Asn Val Leu Asp Ile Pro Pro
 115 120 125
 Asn Ser Pro Glu Gln Glu Gly Lys Asn Ala Leu Lys Phe Ala Met Gln
 130 135 140
 Asn Arg Ile Lys Leu Phe Tyr Arg Pro Ala Gly Ile Ala Pro Val Asn
 145 150 155 160
 Lys Ala Thr Phe Lys Lys Leu Leu Val Asn Arg Ser Gly Asn Gly Leu
 165 170 175
 Val Ile Lys Asn Asp Ser Ala Asn Trp Val Thr Ile Ser Asp Val Lys
 180 185 190
 Ala Asn Asn Val Lys Val Asn Tyr Glu Thr Ile Met Ile Ala Pro Leu

				85					90					95					
Glu	Asn	Met	Thr	Pro	Phe	Met	Tyr	Val	Leu	Asn	Thr	Pro	Pro	Val	Ile				
			100					105						110					

<210> 290
 <211> 193
 <212> PRT
 <213> E. Coli

<400> 290

Met	Thr	Asp	Tyr	Leu	Leu	Leu	Phe	Val	Gly	Thr	Val	Leu	Val	Asn	Asn				
1				5					10					15					
Phe	Val	Leu	Val	Lys	Phe	Leu	Gly	Leu	Cys	Pro	Phe	Met	Gly	Val	Ser				
			20					25					30						
Lys	Lys	Leu	Glu	Thr	Ala	Met	Gly	Met	Gly	Leu	Ala	Thr	Thr	Phe	Val				
			35				40					45							
Met	Thr	Leu	Ala	Ser	Ile	Cys	Ala	Trp	Leu	Ile	Asp	Thr	Trp	Ile	Leu				
			50			55					60								
Ile	Pro	Leu	Asn	Leu	Ile	Tyr	Leu	Arg	Thr	Leu	Ala	Phe	Ile	Leu	Val				
65					70				75						80				
Ile	Ala	Val	Val	Val	Gln	Phe	Thr	Glu	Met	Val	Val	Arg	Lys	Thr	Ser				
				85					90					95					
Pro	Val	Leu	Tyr	Arg	Leu	Leu	Gly	Ile	Phe	Leu	Pro	Leu	Ile	Thr	Thr				
			100					105						110					
Asn	Cys	Ala	Val	Leu	Gly	Val	Ala	Leu	Leu	Asn	Ile	Asn	Leu	Gly	His				
		115					120					125							
Asn	Phe	Leu	Gln	Ser	Ala	Leu	Tyr	Gly	Phe	Ser	Ala	Ala	Val	Gly	Phe				
		130				135					140								
Ser	Leu	Val	Met	Val	Leu	Phe	Ala	Ala	Ile	Arg	Glu	Arg	Leu	Ala	Val				
145					150				155						160				
Ala	Asp	Val	Pro	Ala	Pro	Phe	Arg	Gly	Asn	Ala	Ile	Ala	Leu	Ile	Thr				
				165				170						175					
Ala	Gly	Leu	Met	Ser	Leu	Ala	Phe	Met	Gly	Phe	Ser	Gly	Leu	Val	Lys				
			180					185						190					

Leu

<210> 291
 <211> 192
 <212> PRT
 <213> E. Coli

<400> 291

Met	Asn	Ala	Ile	Trp	Ile	Ala	Val	Ala	Ala	Val	Ser	Leu	Leu	Gly	Leu				
1				5				10						15					
Ala	Phe	Gly	Ala	Ile	Leu	Gly	Tyr	Ala	Ser	Arg	Arg	Phe	Ala	Val	Glu				
			20					25					30						
Asp	Asp	Pro	Val	Val	Glu	Lys	Ile	Asp	Glu	Ile	Leu	Pro	Gln	Ser	Gln				
			35				40					45							
Cys	Gly	Gln	Cys	Gly	Tyr	Pro	Gly	Cys	Arg	Pro	Tyr	Ala	Glu	Ala	Ile				
		50				55					60								
Ser	Cys	Asn	Gly	Glu	Lys	Ile	Asn	Arg	Cys	Ala	Pro	Gly	Gly	Glu	Ala				
65					70				75					80					
Val	Met	Leu	Lys	Ile	Ala	Glu	Leu	Leu	Asn	Val	Glu	Pro	Gln	Pro	Leu				

Gly	Glu	Pro	Ile	Thr	Glu	Arg	Val	Val	Thr	Leu	Thr	Gly	Glu	Ala	Ile
290						295					300				
Ala	Arg	Pro	Gly	Asn	Val	Trp	Ala	Arg	Leu	Gly	Thr	Pro	Val	Arg	His
305				310						315					320
Leu	Leu	Asn	Asp	Ala	Gly	Phe	Cys	Pro	Ser	Ala	Asp	Gln	Met	Val	Ile
			325					330						335	
Met	Gly	Gly	Pro	Leu	Met	Gly	Phe	Thr	Leu	Pro	Trp	Leu	Asp	Val	Pro
			340					345					350		
Val	Val	Lys	Ile	Thr	Asn	Cys	Leu	Leu	Ala	Pro	Ser	Ala	Asn	Glu	Leu
		355					360					365			
Gly	Glu	Pro	Gln	Glu	Glu	Gln	Ser	Cys	Ile	Arg	Cys	Ser	Ala	Cys	Ala
	370					375					380				
Asp	Ala	Cys	Pro	Ala	Asp	Leu	Leu	Pro	Gln	Gln	Leu	Tyr	Trp	Phe	Ser
385					390					395					400
Lys	Gly	Gln	Gln	His	Asp	Lys	Ala	Thr	Thr	His	Asn	Ile	Ala	Asp	Cys
				405					410					415	
Ile	Glu	Cys	Gly	Ala	Cys	Ala	Trp	Val	Cys	Pro	Ser	Asn	Ile	Pro	Leu
			420					425					430		
Val	Gln	Tyr	Phe	Arg	Gln	Glu	Lys	Ala	Glu	Ile	Ala	Ala	Ile	Arg	Gln
		435					440					445			
Glu	Glu	Lys	Arg	Ala	Ala	Glu	Ala	Lys	Ala	Arg	Phe	Glu	Ala	Arg	Gln
	450					455					460				
Ala	Arg	Leu	Glu	Arg	Glu	Lys	Ala	Ala	Arg	Leu	Glu	Arg	His	Lys	Ser
465					470					475					480
Ala	Ala	Val	Gln	Pro	Ala	Ala	Lys	Asp	Lys	Asp	Ala	Ile	Ala	Ala	Ala
				485					490					495	
Leu	Ala	Arg	Val	Lys	Glu	Lys	Gln	Ala	Gln	Ala	Thr	Gln	Pro	Ile	Val
			500					505					510		
Ile	Lys	Ala	Gly	Glu	Arg	Pro	Asp	Asn	Ser	Ala	Ile	Ile	Ala	Ala	Arg
		515					520					525			
Glu	Ala	Arg	Lys	Ala	Gln	Ala	Arg	Ala	Lys	Gln	Ala	Glu	Leu	Gln	Gln
	530					535					540				
Thr	Asn	Asp	Ala	Ala	Thr	Val	Ala	Asp	Pro	Arg	Lys	Thr	Ala	Val	Glu
545					550					555					560
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
				565					570					575	
Asn	Ala	Glu	Pro	Glu	Gln	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
			580					585					590		
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
		595					600					605			
Asn	Ala	Glu	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
	610					615					620				
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
625					630					635					640
Asn	Ala	Glu	Pro	Glu	Gln	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
				645					650					655	
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Arg	Glu	Gln	Gln	Pro	Ala
			660					665					670		
Asn	Ala	Glu	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Glu
		675				680						685			
Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Arg	Lys	Leu	Glu	Gln	Gln	Gln	Ala
	690					695					700				
Asn	Ala	Val	Pro	Glu	Glu	Gln	Val	Asp	Pro	Arg	Lys	Ala	Ala	Val	Ala
705					710					715					720
Ala	Ala	Ile	Ala	Arg	Ala	Gln	Ala	Lys	Lys	Ala	Ala	Gln	Gln	Lys	Val
				725					730					735	
Val	Asn	Glu	Asp												

740

<210> 293
 <211> 352
 <212> PRT
 <213> E. Coli

<400> 293
 Met Val Phe Arg Ile Ala Ser Ser Pro Tyr Thr His Asn Gln Arg Gln
 1 5 10 15
 Thr Ser Arg Ile Met Leu Leu Val Leu Leu Ala Ala Val Pro Gly Ile
 20 25 30
 Ala Ala Gln Leu Trp Phe Phe Gly Trp Gly Thr Leu Val Gln Ile Leu
 35 40 45
 Leu Ala Ser Val Ser Ala Leu Leu Ala Glu Ala Leu Val Leu Lys Leu
 50 55 60
 Arg Lys Gln Ser Val Ala Ala Thr Leu Lys Asp Asn Ser Ala Leu Leu
 65 70 75 80
 Thr Gly Leu Leu Leu Ala Val Ser Ile Pro Pro Leu Ala Pro Trp Trp
 85 90 95
 Met Val Val Leu Gly Thr Val Phe Ala Val Ile Ile Ala Lys Gln Leu
 100 105 110
 Tyr Gly Gly Leu Gly Gln Asn Pro Phe Asn Pro Ala Met Ile Gly Tyr
 115 120 125
 Val Val Leu Leu Ile Ser Phe Pro Val Gln Met Thr Ser Trp Leu Pro
 130 135 140
 Pro His Glu Ile Ala Val Asn Ile Pro Gly Phe Ile Asp Ala Ile Gln
 145 150 155 160
 Val Ile Phe Ser Gly His Thr Ala Ser Gly Gly Asp Met Asn Thr Leu
 165 170 175
 Arg Leu Gly Ile Asp Gly Ile Ser Gln Ala Thr Pro Leu Asp Thr Phe
 180 185 190
 Lys Thr Ser Val Arg Ala Gly His Ser Val Glu Gln Ile Met Gln Tyr
 195 200 205
 Pro Ile Tyr Ser Gly Ile Leu Ala Gly Ala Gly Trp Gln Trp Val Asn
 210 215 220
 Leu Ala Trp Leu Ala Gly Gly Val Trp Leu Leu Trp Gln Lys Ala Ile
 225 230 235 240
 Arg Trp His Ile Pro Leu Ser Phe Leu Val Thr Leu Ala Leu Cys Ala
 245 250 255
 Met Leu Gly Trp Leu Phe Ser Pro Glu Thr Leu Ala Ala Pro Gln Ile
 260 265 270
 His Leu Leu Ser Gly Ala Thr Met Leu Gly Ala Phe Phe Ile Leu Thr
 275 280 285
 Asp Pro Val Thr Ala Ser Thr Thr Asn Arg Gly Arg Leu Ile Phe Gly
 290 295 300
 Ala Leu Ala Gly Leu Leu Val Trp Leu Ile Arg Ser Phe Gly Gly Tyr
 305 310 315 320
 Pro Asp Gly Val Ala Phe Ala Val Leu Leu Ala Asn Ile Thr Val Pro
 325 330 335
 Leu Ile Asp Tyr Tyr Thr Arg Pro Arg Val Tyr Gly His Arg Lys Gly
 340 345 350

<210> 294

<211> 206
 <212> PRT
 <213> E. Coli

<400> 294
 Met Leu Lys Thr Ile Arg Lys His Gly Ile Thr Leu Ala Leu Phe Ala
 1 5 10 15
 Ala Gly Ser Thr Gly Leu Thr Ala Ala Ile Asn Gln Met Thr Lys Thr
 20 25 30
 Thr Ile Ala Glu Gln Ala Ser Leu Gln Gln Lys Ala Leu Phe Asp Gln
 35 40 45
 Val Leu Pro Ala Glu Arg Tyr Asn Asn Ala Leu Ala Gln Ser Cys Tyr
 50 55 60
 Leu Val Thr Ala Pro Glu Leu Gly Lys Gly Glu His Arg Val Tyr Ile
 65 70 75 80
 Ala Lys Gln Asp Asp Lys Pro Val Ala Ala Val Leu Glu Ala Thr Ala
 85 90 95
 Pro Asp Gly Tyr Ser Gly Ala Ile Gln Leu Leu Val Gly Ala Asp Phe
 100 105 110
 Asn Gly Thr Val Leu Gly Thr Arg Val Thr Glu His His Glu Thr Pro
 115 120 125
 Gly Leu Gly Asp Lys Ile Glu Leu Arg Leu Ser Asp Trp Ile Thr His
 130 135 140
 Phe Ala Gly Lys Lys Ile Ser Gly Ala Asp Asp Ala His Trp Ala Val
 145 150 155 160
 Lys Lys Asp Gly Gly Asp Phe Asp Gln Phe Thr Gly Ala Thr Ile Thr
 165 170 175
 Pro Arg Ala Val Val Asn Ala Val Lys Arg Ala Gly Leu Tyr Ala Gln
 180 185 190
 Thr Leu Pro Ala Gln Leu Ser Gln Leu Pro Ala Cys Gly Glu
 195 200 205

<210> 295
 <211> 231
 <212> PRT
 <213> E. Coli

<400> 295
 Met Ser Glu Ile Lys Asp Val Ile Val Gln Gly Leu Trp Lys Asn Asn
 1 5 10 15
 Ser Ala Leu Val Gln Leu Leu Gly Leu Cys Pro Leu Leu Ala Val Thr
 20 25 30
 Ser Thr Ala Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr Thr Leu Val
 35 40 45
 Leu Thr Leu Thr Asn Leu Thr Ile Ser Thr Leu Arg His Trp Thr Pro
 50 55 60
 Ala Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala Ser Val Val
 65 70 75 80
 Ser Ala Val Gln Met Leu Ile Asn Ala Tyr Ala Phe Gly Leu Tyr Gln
 85 90 95
 Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys Ile Val Val
 100 105 110
 Gly Arg Ala Glu Ala Phe Ala Ala Lys Lys Gly Pro Ala Leu Ser Ala
 115 120 125
 Leu Asp Gly Phe Ser Ile Gly Met Gly Ala Thr Cys Ala Met Phe Val
 130 135 140

Leu Gly Ser Leu Arg Glu Ile Ile Gly Asn Gly Thr Leu Phe Asp Gly
 145 150 155 160
 Ala Asp Ala Leu Leu Gly Ser Trp Ala Lys Val Leu Arg Val Glu Ile
 165 170 175
 Phe His Thr Asp Ser Pro Phe Leu Leu Ala Met Leu Pro Pro Gly Ala
 180 185 190
 Phe Ile Gly Leu Gly Leu Met Leu Ala Gly Lys Tyr Leu Ile Asp Glu
 195 200 205
 Arg Met Lys Lys Arg Arg Ala Glu Ala Ala Ala Glu Arg Ala Leu Pro
 210 215 220
 Asn Gly Glu Thr Gly Asn Val
 225 230

<210> 296
 <211> 211
 <212> PRT
 <213> E. Coli

<400> 296
 Met Asn Lys Ala Lys Arg Leu Glu Ile Leu Thr Arg Leu Arg Glu Asn
 1 5 10 15
 Asn Pro His Pro Thr Thr Glu Leu Asn Phe Ser Ser Pro Phe Glu Leu
 20 25 30
 Leu Ile Ala Val Leu Leu Ser Ala Gln Ala Thr Asp Val Ser Val Asn
 35 40 45
 Lys Ala Thr Ala Lys Leu Tyr Pro Val Ala Asn Thr Pro Ala Ala Met
 50 55 60
 Leu Glu Leu Gly Val Glu Gly Val Lys Thr Tyr Ile Lys Thr Ile Gly
 65 70 75 80
 Leu Tyr Asn Ser Lys Ala Glu Asn Ile Ile Lys Thr Cys Arg Ile Leu
 85 90 95
 Leu Glu Gln His Asn Gly Glu Val Pro Glu Asp Arg Ala Ala Leu Glu
 100 105 110
 Ala Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val Val Leu Asn Thr
 115 120 125
 Ala Phe Gly Trp Pro Thr Ile Ala Val Asp Thr His Ile Phe Arg Val
 130 135 140
 Cys Asn Arg Thr Gln Phe Ala Pro Gly Lys Asn Val Glu Gln Val Glu
 145 150 155 160
 Glu Lys Leu Leu Lys Val Val Pro Ala Glu Phe Lys Val Asp Cys His
 165 170 175
 His Trp Leu Ile Leu His Gly Arg Tyr Thr Cys Ile Ala Arg Lys Pro
 180 185 190
 Arg Cys Gly Ser Cys Ile Ile Glu Asp Leu Cys Glu Tyr Lys Glu Lys
 195 200 205
 Val Asp Ile
 210

<210> 297
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 297
 Met Lys Arg Leu His Lys Arg Phe Leu Leu Ala Thr Phe Cys Ala Leu

1		5		10		15									
Phe	Thr	Ala	Thr	Leu	Gln	Ala	Ala	Asp	Val	Thr	Ile	Thr	Val	Asn	Gly
		20						25					30		
Arg	Val	Val	Ala	Lys	Pro	Cys	Thr	Ile	Gln	Thr	Lys	Glu	Ala	Asn	Val
		35					40					45			
Asn	Leu	Gly	Asp	Leu	Tyr	Thr	Arg	Asn	Leu	Gln	Gln	Pro	Gly	Ser	Ala
	50					55					60				
Ser	Gly	Trp	His	Asn	Ile	Thr	Leu	Ser	Leu	Thr	Asp	Cys	Pro	Val	Glu
65					70					75					80
Thr	Ser	Ala	Val	Thr	Ala	Ile	Val	Thr	Gly	Ser	Thr	Asp	Asn	Thr	Gly
				85					90					95	
Tyr	Tyr	Lys	Asn	Glu	Gly	Thr	Ala	Glu	Asn	Ile	Gln	Ile	Glu	Leu	Arg
			100					105					110		
Asp	Asp	Gln	Asp	Ala	Ala	Leu	Lys	Asn	Gly	Asp	Ser	Lys	Thr	Val	Ile
		115					120					125			
Val	Asp	Glu	Ile	Thr	Arg	Asn	Ala	Gln	Phe	Pro	Leu	Lys	Ala	Arg	Ala
	130					135					140				
Ile	Thr	Val	Asn	Gly	Asn	Ala	Ser	Gln	Gly	Thr	Ile	Glu	Ala	Leu	Ile
145					150					155					160
Asn	Val	Ile	Tyr	Thr	Trp	Gln									
				165											

<210> 298

<211> 176

<212> PRT

<213> E. Coli

<400> 298

Met	Lys	Tyr	Asn	Asn	Ile	Ile	Phe	Leu	Gly	Leu	Cys	Leu	Gly	Leu	Thr
1				5					10					15	
Thr	Tyr	Ser	Ala	Leu	Ser	Ala	Asp	Ser	Val	Ile	Lys	Ile	Ser	Gly	Arg
			20					25					30		
Val	Leu	Asp	Tyr	Gly	Cys	Thr	Val	Ser	Ser	Asp	Ser	Leu	Asn	Phe	Thr
		35				40						45			
Val	Asp	Leu	Gln	Lys	Asn	Ser	Ala	Arg	Gln	Phe	Pro	Thr	Thr	Gly	Ser
	50				55						60				
Thr	Ser	Pro	Ala	Val	Pro	Phe	Gln	Ile	Thr	Leu	Ser	Glu	Cys	Ser	Lys
65					70					75					80
Gly	Thr	Thr	Gly	Val	Arg	Val	Ala	Phe	Asn	Gly	Ile	Glu	Asp	Ala	Glu
				85					90					95	
Asn	Asn	Thr	Leu	Leu	Lys	Leu	Asp	Glu	Gly	Ser	Asn	Thr	Ala	Ser	Gly
			100					105					110		
Leu	Gly	Ile	Glu	Ile	Leu	Asp	Ala	Asn	Met	Arg	Pro	Val	Lys	Leu	Asn
		115					120					125			
Asp	Leu	His	Ala	Gly	Met	Gln	Trp	Ile	Pro	Leu	Val	Pro	Glu	Gln	Asn
	130					135					140				
Asn	Ile	Leu	Pro	Tyr	Ser	Ala	Arg	Leu	Lys	Ser	Thr	Gln	Lys	Ser	Val
145					150					155					160
Asn	Pro	Gly	Leu	Val	Arg	Ala	Ser	Ala	Thr	Phe	Thr	Leu	Glu	Phe	Gln
				165					170					175	

<210> 299

<211> 382

<212> PRT

<213> E. Coli

<400> 299

Met	Ser	Gly	Tyr	Thr	Val	Lys	Pro	Pro	Thr	Gly	Asp	Thr	Asn	Glu	Gln
1				5					10					15	
Thr	Gln	Phe	Ile	Asp	Tyr	Phe	Asn	Leu	Phe	Tyr	Ser	Lys	Arg	Gly	Gln
			20					25					30		
Glu	Gln	Ile	Ser	Ile	Ser	Gln	Gln	Leu	Gly	Asn	Tyr	Gly	Thr	Thr	Phe
		35					40					45			
Phe	Ser	Ala	Ser	Arg	Gln	Ser	Tyr	Trp	Asn	Thr	Ser	Arg	Ser	Asp	Gln
	50					55					60				
Gln	Ile	Ser	Phe	Gly	Leu	Asn	Val	Pro	Phe	Gly	Asp	Ile	Thr	Thr	Ser
65					70					75					80
Leu	Asn	Tyr	Ser	Tyr	Ser	Asn	Asn	Ile	Trp	Gln	Asn	Asp	Arg	Asp	His
			85						90					95	
Leu	Leu	Ala	Phe	Thr	Leu	Asn	Val	Pro	Phe	Ser	His	Trp	Met	Arg	Thr
		100						105					110		
Asp	Ser	Gln	Ser	Ala	Phe	Arg	Asn	Ser	Asn	Ala	Ser	Tyr	Ser	Met	Ser
	115						120					125			
Asn	Asp	Leu	Lys	Gly	Gly	Met	Thr	Asn	Leu	Ser	Gly	Val	Tyr	Gly	Thr
	130					135					140				
Leu	Leu	Pro	Asp	Asn	Asn	Leu	Asn	Tyr	Ser	Val	Gln	Val	Gly	Asn	Thr
145					150					155					160
His	Gly	Gly	Asn	Thr	Ser	Ser	Gly	Thr	Ser	Gly	Tyr	Ser	Ser	Leu	Asn
			165						170					175	
Tyr	Arg	Gly	Ala	Tyr	Gly	Asn	Thr	Asn	Val	Gly	Tyr	Ser	Arg	Ser	Gly
		180						185					190		
Asp	Ser	Ser	Gln	Ile	Tyr	Tyr	Gly	Met	Ser	Gly	Gly	Ile	Ile	Ala	His
	195						200					205			
Ala	Asp	Gly	Ile	Thr	Phe	Gly	Gln	Pro	Leu	Gly	Asp	Thr	Met	Val	Leu
	210					215					220				
Val	Lys	Ala	Pro	Gly	Ala	Asp	Asn	Val	Lys	Ile	Glu	Asn	Gln	Thr	Gly
225					230					235					240
Ile	His	Thr	Asp	Trp	Arg	Gly	Tyr	Ala	Ile	Leu	Pro	Phe	Ala	Thr	Glu
			245					250						255	
Tyr	Arg	Glu	Asn	Arg	Val	Ala	Leu	Asn	Ala	Asn	Ser	Leu	Ala	Asp	Asn
		260					265						270		
Val	Glu	Leu	Asp	Glu	Thr	Val	Val	Thr	Val	Ile	Pro	Thr	His	Gly	Ala
	275					280						285			
Ile	Ala	Arg	Ala	Thr	Phe	Asn	Ala	Gln	Ile	Gly	Gly	Lys	Val	Leu	Met
	290					295					300				
Thr	Leu	Lys	Tyr	Gly	Asn	Lys	Ser	Val	Pro	Phe	Gly	Ala	Ile	Val	Thr
305					310					315					320
His	Gly	Glu	Asn	Lys	Asn	Gly	Ser	Ile	Val	Ala	Glu	Asn	Gly	Gln	Val
			325						330					335	
Tyr	Leu	Thr	Gly	Leu	Pro	Gln	Ser	Gly	Gln	Leu	Gln	Val	Ser	Trp	Gly
		340					345						350		
Lys	Asp	Lys	Asn	Ser	Asn	Cys	Ile	Val	Glu	Tyr	Lys	Leu	Pro	Glu	Val
	355					360						365			
Ser	Pro	Gly	Thr	Leu	Leu	Asn	Gln	Gln	Thr	Ala	Ile	Cys	Arg		
	370					375						380			

<210> 300

<211> 138

<212> PRT

<213> E. Coli

<400> 300

```
Met Ile Ala Ile Ala Asp Ile Leu Gln Ala Gly Glu Lys Leu Thr Ala
 1           5           10           15
Val Ala Pro Phe Leu Ala Gly Ile Gln Asn Glu Glu Gln Tyr Thr Gln
          20           25           30
Ala Leu Glu Leu Val Asp His Leu Leu Asn Asp Pro Glu Asn Pro
      35           40           45
Leu Leu Asp Leu Val Cys Ala Lys Ile Thr Ala Trp Glu Glu Ser Ala
      50           55           60
Pro Glu Phe Ala Glu Phe Asn Ala Met Ala Gln Ala Met Pro Gly Gly
65           70           75           80
Ile Ala Val Ile Arg Thr Leu Met Asp Gln Tyr Gly Leu Thr Leu Ser
          85           90           95
Asp Leu Pro Glu Ile Gly Ser Lys Ser Met Val Ser Arg Val Leu Ser
          100          105          110
Gly Lys Arg Lys Leu Thr Leu Glu His Ala Lys Lys Leu Ala Thr Arg
      115           120          125
Phe Gly Ile Ser Pro Ala Leu Phe Ile Asp
130           135
```

<210> 301

<211> 104

<212> PRT

<213> E. Coli

<400> 301

```
Met His Leu Ile Thr Gln Lys Ala Leu Lys Asp Ala Ala Glu Lys Tyr
 1           5           10           15
Pro Gln His Lys Thr Glu Leu Val Ala Leu Gly Asn Thr Ile Ala Lys
          20           25           30
Gly Tyr Phe Lys Lys Pro Glu Ser Leu Lys Ala Val Phe Pro Ser Leu
      35           40           45
Asp Asn Phe Lys Tyr Leu Asp Lys His Tyr Val Phe Asn Val Gly Gly
      50           55           60
Asn Glu Leu Arg Val Val Ala Met Val Phe Phe Glu Ser Gln Lys Cys
65           70           75           80
Tyr Ile Arg Glu Val Met Thr His Lys Glu Tyr Asp Phe Phe Thr Ala
          85           90           95
Val His Arg Thr Lys Gly Lys Lys
          100
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<210> 302

<211> 2383

<212> PRT

<213> E. Coli

<400> 302

```
Met Leu Ser Val Phe Thr Phe Phe Arg Cys Ala Arg Lys Gly Ala Phe
 1           5           10           15
Met Leu Ala Arg Ser Gly Lys Val Ser Met Ala Thr Lys Lys Arg Ser
          20           25           30
Gly Glu Glu Ile Asn Asp Arg Gln Ile Leu Cys Gly Met Gly Ile Lys
```


Ala	Gly	Gly	Lys	Val	Val	Thr	Thr	Gly	Lys	Asp	Ile	Leu	Val	Thr	Leu
			500					505					510		
Pro	Ala	Tyr	Arg	Phe	Thr	Ser	Thr	Pro	Glu	Thr	Asp	Asn	Thr	Trp	Pro
		515					520					525			
Ile	Glu	Val	Thr	Ala	Glu	Asp	Val	Lys	Gly	Asn	Leu	Ser	Asn	Arg	Glu
	530					535					540				
Gln	Ser	Met	Val	Val	Val	Gln	Ala	Pro	Thr	Leu	Ser	Gln	Lys	Asp	Ser
545					550					555					560
Ser	Val	Ser	Leu	Ser	Thr	Gln	Thr	Leu	Asn	Ala	Asp	Ser	His	Ser	Thr
				565					570					575	
Ala	Thr	Leu	Thr	Phe	Ile	Ala	His	Asp	Ala	Ala	Gly	Asn	Pro	Val	Val
			580					585					590		
Gly	Leu	Val	Leu	Ser	Thr	Arg	His	Glu	Gly	Val	Gln	Asp	Ile	Thr	Leu
	595					600						605			
Ser	Asp	Trp	Lys	Asp	Asn	Gly	Asp	Gly	Ser	Tyr	Thr	Gln	Ile	Leu	Thr
	610					615					620				
Thr	Gly	Ala	Met	Ser	Gly	Thr	Leu	Thr	Leu	Met	Pro	Gln	Leu	Asn	Gly
625					630					635					640
Val	Asp	Ala	Ala	Lys	Ala	Pro	Ala	Val	Val	Asn	Ile	Ile	Ser	Val	Ser
				645					650					655	
Ser	Ser	Arg	Thr	His	Ser	Ser	Ile	Lys	Ile	Asp	Lys	Asp	Arg	Tyr	Leu
			660					665					670		
Ser	Gly	Asn	Pro	Ile	Glu	Val	Thr	Val	Glu	Leu	Arg	Asp	Glu	Asn	Asp
	675						680					685			
Lys	Pro	Val	Lys	Glu	Gln	Lys	Gln	Gln	Leu	Asn	Asn	Ala	Val	Ser	Ile
	690					695					700				
Asp	Asn	Val	Lys	Pro	Gly	Val	Thr	Thr	Asp	Trp	Lys	Glu	Thr	Ala	Asp
705					710					715					720
Gly	Val	Tyr	Lys	Ala	Thr	Tyr	Thr	Ala	Tyr	Thr	Lys	Gly	Ser	Gly	Leu
			725					730						735	
Thr	Ala	Lys	Leu	Leu	Met	Gln	Asn	Trp	Asn	Glu	Asp	Leu	His	Thr	Ala
	740						745						750		
Gly	Phe	Ile	Ile	Asp	Ala	Asn	Pro	Gln	Ser	Ala	Lys	Ile	Ala	Thr	Leu
	755						760					765			
Ser	Ala	Ser	Asn	Asn	Gly	Val	Leu	Ala	Asn	Glu	Asn	Ala	Ala	Asn	Thr
	770					775					780				
Val	Ser	Val	Asn	Val	Ala	Asp	Glu	Gly	Ser	Asn	Pro	Ile	Asn	Asp	His
785					790					795					800
Thr	Val	Thr	Phe	Ala	Val	Leu	Ser	Gly	Ser	Ala	Thr	Ser	Phe	Asn	Asn
			805					810						815	
Gln	Asn	Thr	Ala	Lys	Thr	Asp	Val	Asn	Gly	Leu	Ala	Thr	Phe	Asp	Leu
			820					825					830		
Lys	Ser	Ser	Lys	Gln	Glu	Asp	Asn	Thr	Val	Glu	Val	Thr	Leu	Glu	Asn
	835						840					845			
Gly	Val	Lys	Gln	Thr	Leu	Ile	Val	Ser	Phe	Val	Gly	Asp	Ser	Ser	Thr
	850					855					860				
Ala	Gln	Val	Asp	Leu	Gln	Lys	Ser	Lys	Asn	Glu	Val	Val	Ala	Asp	Gly
865					870					875					880
Asn	Asp	Ser	Val	Thr	Met	Thr	Ala	Thr	Val	Arg	Asp	Ala	Lys	Gly	Asn
			885					890						895	
Leu	Leu	Asn	Asp	Val	Met	Val	Thr	Phe	Asn	Val	Asn	Ser	Ala	Glu	Ala
			900					905					910		
Lys	Leu	Ser	Gln	Thr	Glu	Val	Asn	Ser	His	Asp	Gly	Ile	Ala	Thr	Ala
	915						920					925			
Thr	Leu	Thr	Ser	Leu	Lys	Asn	Gly	Asp	Tyr	Arg	Val	Thr	Ala	Ser	Val
	930					935					940				
Ser	Ser	Gly	Ser	Gln	Ala	Asn	Gln	Gln	Val	Asn	Phe	Ile	Gly	Asp	Gln

945		950		955		960
Ser Thr Ala Ala	Leu Thr Leu Ser Val	Pro Ser Gly Asp Ile Thr Val				
	965	970		975		
Thr Asn Thr Ala	Pro Gln Tyr Met Thr	Ala Thr Leu Gln Asp Lys Asn				
	980	985		990		
Gly Asn Pro Leu	Lys Asp Lys Glu Ile Thr	Phe Ser Val Pro Asn Asp				
	995	1000		1005		
Val Ala Ser Lys	Phe Ser Ile Ser Asn Gly	Gly Lys Gly Met Thr Asp				
	1010	1015		1020		
Ser Asn Gly Val	Ala Ile Ala Ser Leu Thr	Gly Thr Leu Ala Gly Thr				
1025	1030	1035		1040		
His Met Ile Met	Ala Arg Leu Ala Asn Ser	Asn Val Ser Asp Ala Gln				
	1045	1050		1055		
Pro Met Thr Phe	Val Ala Asp Lys Asp Arg	Ala Val Val Val Leu Gln				
	1060	1065		1070		
Thr Ser Lys Ala	Glu Ile Ile Gly Asn Gly	Val Asp Glu Thr Thr Leu				
	1075	1080		1085		
Thr Ala Thr Val	Lys Asp Pro Ser Asn His	Pro Val Ala Gly Ile Thr				
	1090	1095		1100		
Val Asn Phe Thr	Met Pro Gln Asp Val Ala	Asn Phe Thr Leu Glu				
1105	1110	1115		1120		
Asn Asn Gly Ile	Ala Ile Thr Gln Ala Asn	Gly Glu Ala His Val Thr				
	1125	1130		1135		
Leu Lys Gly Lys	Lys Ala Gly Thr His Thr	Val Thr Ala Thr Leu Gly				
	1140	1145		1150		
Asn Asn Asn Thr	Ser Asp Ser Gln Pro Val	Thr Phe Val Ala Asp Lys				
	1155	1160		1165		
Ala Ser Ala Gln	Val Val Leu Gln Ile Ser	Lys Asp Glu Ile Thr Gly				
	1170	1175		1180		
Asn Gly Val Asp	Ser Ala Thr Leu Thr Ala	Thr Val Lys Asp Gln Phe				
1185	1190	1195		1200		
Asp Asn Glu Val	Asn Asn Leu Pro Val Thr	Phe Ser Ser Ala Ser Ser				
	1205	1210		1215		
Gly Leu Thr Leu	Thr Pro Gly Val Ser Asn	Thr Asn Glu Ser Gly Ile				
	1220	1225		1230		
Ala Gln Ala Thr	Leu Ala Gly Val Ala Phe	Gly Glu Lys Thr Val Thr				
	1235	1240		1245		
Ala Ser Leu Ala	Asn Asn Gly Ala Ser Asp	Asn Lys Thr Val His Phe				
	1250	1255		1260		
Ile Gly Asp Thr	Ala Ala Lys Ile Ile Glu	Leu Ala Pro Val Pro				
1265	1270	1275		1280		
Asp Ser Ile Ile	Ala Gly Thr Pro Gln Asn	Ser Ser Gly Ser Val Ile				
	1285	1290		1295		
Thr Ala Thr Val	Val Asp Asn Asn Gly Phe	Pro Val Lys Gly Val Thr				
	1300	1305		1310		
Val Asn Phe Thr	Ser Asn Ala Ala Thr Ala	Glu Met Thr Asn Gly Gly				
	1315	1320		1325		
Gln Ala Val Thr	Asn Glu Gln Gly Lys Ala	Thr Val Thr Tyr Thr Asn				
	1330	1335		1340		
Thr Arg Ser Ser	Ile Glu Ser Gly Ala Arg	Pro Asp Thr Val Glu Ala				
1345	1350	1355		1360		
Ser Leu Glu Asn	Gly Ser Ser Thr Leu Ser	Thr Ser Ile Asn Val Asn				
	1365	1370		1375		
Ala Asp Ala Ser	Thr Ala His Leu Thr Leu	Leu Gln Ala Leu Phe Asp				
	1380	1385		1390		
Thr Val Ser Ala	Gly Glu Thr Thr Ser Leu	Tyr Ile Glu Val Lys Asp				
	1395	1400		1405		

Asn Tyr Gly Asn Gly Val Pro Gln Gln Glu Val Thr Leu Ser Val Ser
 1410 1415 1420
 Pro Ser Glu Gly Val Thr Pro Ser Asn Asn Ala Ile Tyr Thr Thr Asn
 1425 1430 1435 1440
 His Asp Gly Asn Phe Tyr Ala Ser Phe Thr Ala Thr Lys Ala Gly Val
 1445 1450 1455
 Tyr Gln Leu Thr Ala Thr Leu Glu Asn Gly Asp Ser Met Gln Gln Thr
 1460 1465 1470
 Val Thr Tyr Val Pro Asn Val Ala Asn Ala Glu Ile Thr Leu Ala Ala
 1475 1480 1485
 Ser Lys Asp Pro Val Ile Ala Asp Asn Asn Asp Leu Thr Thr Leu Thr
 1490 1495 1500
 Ala Thr Val Ala Asp Thr Glu Gly Asn Ala Ile Ala Asn Thr Glu Val
 1505 1510 1515 1520
 Thr Phe Thr Leu Pro Glu Asp Val Lys Ala Asn Phe Thr Leu Ser Asp
 1525 1530 1535
 Gly Gly Lys Val Ile Thr Asp Ala Glu Gly Lys Ala Lys Val Thr Leu
 1540 1545 1550
 Lys Gly Thr Lys Ala Gly Ala His Thr Val Thr Ala Ser Met Thr Gly
 1555 1560 1565
 Gly Lys Ser Glu Gln Leu Val Val Asn Phe Ile Ala Asp Thr Leu Thr
 1570 1575 1580
 Ala Gln Val Asn Leu Asn Val Thr Glu Asp Asn Phe Ile Ala Asn Asn
 1585 1590 1595 1600
 Val Gly Met Thr Arg Leu Gln Ala Thr Val Thr Asp Gly Asn Gly Asn
 1605 1610 1615
 Pro Leu Ala Asn Glu Ala Val Thr Phe Thr Leu Pro Ala Asp Val Ser
 1620 1625 1630
 Ala Ser Phe Thr Leu Gly Gln Gly Gly Ser Ala Ile Thr Asp Ile Asn
 1635 1640 1645
 Gly Lys Ala Glu Val Thr Leu Ser Gly Thr Lys Ser Gly Thr Tyr Pro
 1650 1655 1660
 Val Thr Val Ser Val Asn Asn Tyr Gly Val Ser Asp Thr Lys Gln Val
 1665 1670 1675 1680
 Thr Leu Ile Ala Asp Ala Gly Thr Ala Lys Leu Ala Ser Leu Thr Ser
 1685 1690 1695
 Val Tyr Ser Phe Val Val Ser Thr Thr Glu Gly Ala Thr Met Thr Ala
 1700 1705 1710
 Ser Val Thr Asp Ala Asn Gly Asn Pro Val Glu Gly Ile Lys Val Asn
 1715 1720 1725
 Phe Arg Gly Thr Ser Val Thr Leu Ser Ser Thr Ser Val Glu Thr Asp
 1730 1735 1740
 Asp Arg Gly Phe Ala Glu Ile Leu Val Thr Ser Thr Glu Val Gly Leu
 1745 1750 1755 1760
 Lys Thr Val Ser Ala Ser Leu Ala Asp Lys Pro Thr Glu Val Ile Ser
 1765 1770 1775
 Arg Leu Leu Asn Ala Ser Ala Asp Val Asn Ser Ala Thr Ile Thr Ser
 1780 1785 1790
 Leu Glu Ile Pro Glu Gly Gln Val Met Val Ala Gln Asp Val Ala Val
 1795 1800 1805
 Lys Ala His Val Asn Asp Gln Phe Gly Asn Pro Val Ala His Gln Pro
 1810 1815 1820
 Val Thr Phe Ser Ala Glu Pro Ser Ser Gln Met Ile Ile Ser Gln Asn
 1825 1830 1835 1840
 Thr Val Ser Thr Asn Thr Gln Gly Val Ala Glu Val Thr Met Thr Pro
 1845 1850 1855
 Glu Arg Asn Gly Ser Tyr Met Val Lys Ala Ser Leu Pro Asn Gly Ala

1860					1865					1870					
Ser	Leu	Glu	Lys	Gln	Leu	Glu	Ala	Ile	Asp	Glu	Lys	Leu	Thr	Leu	Thr
1875					1880					1885					
Ala	Ser	Ser	Pro	Leu	Ile	Gly	Val	Tyr	Ala	Pro	Thr	Gly	Ala	Thr	Leu
1890					1895					1900					
Thr	Ala	Thr	Leu	Thr	Ser	Ala	Asn	Gly	Thr	Pro	Val	Glu	Gly	Gln	Val
1905					1910					1915					
Ile	Asn	Phe	Ser	Val	Thr	Pro	Glu	Gly	Ala	Thr	Leu	Ser	Gly	Gly	Lys
1925					1930					1935					
Val	Arg	Thr	Asn	Ser	Ser	Gly	Gln	Ala	Pro	Val	Val	Leu	Thr	Ser	Asn
1940					1945					1950					
Lys	Val	Gly	Thr	Tyr	Thr	Val	Thr	Ala	Ser	Phe	His	Asn	Gly	Val	Thr
1955					1960					1965					
Ile	Gln	Thr	Gln	Thr	Thr	Val	Lys	Val	Thr	Gly	Asn	Ser	Ser	Thr	Ala
1970					1975					1980					
His	Val	Ala	Ser	Phe	Ile	Ala	Asp	Pro	Ser	Thr	Ile	Ala	Ala	Thr	Asn
1985					1990					1995					
Thr	Asp	Leu	Ser	Thr	Leu	Lys	Ala	Thr	Val	Glu	Asp	Gly	Ser	Gly	Asn
2005					2010					2015					
Leu	Ile	Glu	Gly	Leu	Thr	Val	Tyr	Phe	Ala	Leu	Lys	Ser	Gly	Ser	Ala
2020					2025					2030					
Thr	Leu	Thr	Ser	Leu	Thr	Ala	Val	Thr	Asp	Gln	Asn	Gly	Ile	Ala	Thr
2035					2040					2045					
Thr	Ser	Val	Lys	Gly	Ala	Met	Thr	Gly	Ser	Val	Thr	Val	Ser	Ala	Val
2050					2055					2060					
Thr	Thr	Ala	Gly	Gly	Met	Gln	Thr	Val	Asp	Ile	Thr	Leu	Val	Ala	Gly
2065					2070					2075					
Pro	Ala	Asp	Thr	Ser	Gln	Ser	Val	Leu	Lys	Ser	Asn	Arg	Ser	Ser	Leu
2085					2090					2095					
Lys	Gly	Asp	Tyr	Thr	Asp	Ser	Ala	Glu	Leu	Arg	Leu	Val	Leu	His	Asp
2100					2105					2110					
Ile	Ser	Gly	Asn	Pro	Ile	Lys	Val	Ser	Glu	Gly	Met	Glu	Phe	Val	Gln
2115					2120					2125					
Ser	Gly	Thr	Asn	Val	Pro	Tyr	Ile	Lys	Ile	Ser	Ala	Ile	Asp	Tyr	Ser
2130					2135					2140					
Leu	Asn	Ile	Asn	Gly	Asp	Tyr	Lys	Ala	Thr	Val	Thr	Gly	Gly	Gly	Glu
2145					2150					2155					
Gly	Ile	Ala	Thr	Leu	Ile	Pro	Val	Leu	Asn	Gly	Val	His	Gln	Ala	Gly
2165					2170					2175					
Leu	Ser	Thr	Thr	Ile	Gln	Phe	Thr	Arg	Ala	Glu	Asp	Lys	Ile	Met	Ser
2180					2185					2190					
Gly	Thr	Val	Ser	Val	Asn	Gly	Thr	Asp	Leu	Pro	Thr	Thr	Thr	Phe	Pro
2195					2200					2205					
Ser	Gln	Gly	Phe	Thr	Gly	Ala	Tyr	Tyr	Gln	Leu	Asn	Asn	Asp	Asn	Phe
2210					2215					2220					
Ala	Pro	Gly	Lys	Thr	Ala	Ala	Asp	Tyr	Glu	Phe	Ser	Ser	Ser	Ala	Ser
2225					2230					2235					
Trp	Val	Asp	Val	Asp	Ala	Thr	Gly	Lys	Val	Thr	Phe	Lys	Asn	Val	Gly
2245					2250					2255					
Ser	Asn	Ser	Glu	Arg	Ile	Thr	Ala	Thr	Pro	Lys	Ser	Gly	Gly	Pro	Ser
2260					2265					2270					
Tyr	Val	Tyr	Glu	Ile	Arg	Val	Lys	Ser	Trp	Trp	Val	Asn	Ala	Gly	Glu
2275					2280					2285					
Ala	Phe	Met	Ile	Tyr	Ser	Leu	Ala	Glu	Asn	Phe	Cys	Ser	Ser	Asn	Gly
2290					2295					2300					
Tyr	Thr	Leu	Pro	Arg	Ala	Asn	Tyr	Leu	Asn	His	Cys	Ser	Ser	Arg	Gly
2305					2310					2315					
										2320					

Ile	Gly	Ser	Leu	Tyr	Ser	Glu	Trp	Gly	Asp	Met	Gly	His	Tyr	Thr	Thr
			2325						2330					2335	
Asp	Ala	Gly	Phe	Gln	Ser	Asn	Met	Tyr	Trp	Ser	Ser	Ser	Pro	Ala	Asn
		2340						2345					2350		
Ser	Ser	Glu	Gln	Tyr	Val	Val	Ser	Leu	Ala	Thr	Gly	Asp	Gln	Ser	Val
		2355					2360					2365			
Phe	Glu	Lys	Leu	Gly	Phe	Ala	Tyr	Ala	Thr	Cys	Tyr	Lys	Asn	Leu	
	2370					2375					2380				

<210> 303
 <211> 61
 <212> PRT
 <213> E. Coli

<400> 303															
Met	Ser	Lys	Gly	Ala	Leu	Tyr	Glu	Phe	Asn	Asn	Pro	Asp	Gln	Leu	Lys
1				5					10					15	
Ile	Pro	Leu	Pro	His	Lys	His	Ile	Ala	Ser	Thr	Phe	Asn	Asp	Ile	Met
		20						25					30		
Ser	Lys	Asp	Val	Gly	Tyr	Ala	Tyr	Val	Ser	Leu	Leu	Tyr	Ala	Cys	Pro
		35					40					45			
Leu	Lys	Thr	His	Ser	Leu	Arg	Leu	Asn	Pro	Phe	Ser	Lys			
	50					55					60				

<210> 304
 <211> 398
 <212> PRT
 <213> E. Coli

<400> 304															
Met	Gln	Val	Ala	Glu	Gln	Arg	Ile	Gln	Leu	Ala	Glu	Ala	Gln	Ala	Lys
1				5					10					15	
Ala	Val	Ala	Thr	Gln	Asp	Gly	Pro	Gln	Ile	Asp	Phe	Ser	Ala	Asp	Met
		20						25					30		
Glu	Arg	Gln	Lys	Met	Ser	Ala	Glu	Gly	Leu	Met	Gly	Pro	Phe	Ala	Leu
		35					40					45			
Asn	Asp	Pro	Ala	Ala	Gly	Thr	Gly	Pro	Trp	Tyr	Thr	Asn	Gly	Thr	
	50					55				60					
Phe	Gly	Leu	Thr	Ala	Gly	Trp	His	Leu	Asp	Ile	Trp	Gly	Lys	Asn	Arg
65				70					75					80	
Ala	Glu	Val	Thr	Ala	Arg	Leu	Gly	Thr	Val	Lys	Ala	Arg	Ala	Ala	Glu
				85					90					95	
Arg	Glu	Gln	Thr	Arg	Gln	Leu	Leu	Ala	Gly	Ser	Val	Ala	Arg	Leu	Tyr
		100						105					110		
Trp	Glu	Trp	Gln	Thr	Gln	Ala	Ala	Leu	Asn	Thr	Val	Leu	Gln	Gln	Ile
	115					120						125			
Glu	Lys	Glu	Gln	Asn	Thr	Ile	Ile	Ala	Thr	Asp	Arg	Gln	Leu	Tyr	Gln
	130					135				140					
Asn	Gly	Ile	Thr	Ser	Ser	Val	Glu	Gly	Val	Glu	Thr	Asp	Ile	Asn	Ala
145				150					155					160	
Ser	Lys	Thr	Arg	Gln	Gln	Leu	Asn	Asp	Val	Ala	Gly	Lys	Met	Lys	Ile
				165				170					175		
Ile	Glu	Ala	Arg	Leu	Ser	Ala	Leu	Thr	Asn	Asn	Gln	Thr	Lys	Ser	Leu
		180					185					190			
Lys	Leu	Lys	Pro	Val	Ala	Leu	Pro	Lys	Val	Ala	Ser	Gln	Leu	Pro	Asp

	195		200		205										
Glu	Leu	Gly	Tyr	Ser	Leu	Leu	Ala	Arg	Arg	Ala	Asp	Leu	Gln	Ala	Ala
	210					215					220				
His	Trp	Tyr	Val	Glu	Ser	Ser	Leu	Ser	Thr	Ile	Asp	Ala	Ala	Lys	Ala
225					230					235					240
Ala	Phe	Tyr	Pro	Asp	Ile	Asn	Leu	Met	Ala	Phe	Leu	Gln	Gln	Asp	Ala
				245					250					255	
Leu	His	Leu	Ser	Asp	Leu	Phe	Arg	His	Ser	Ala	Gln	Gln	Met	Gly	Val
			260					265					270		
Thr	Ala	Gly	Leu	Thr	Leu	Pro	Ile	Phe	Asp	Ser	Gly	Arg	Leu	Asn	Ala
	275						280					285			
Asn	Leu	Asp	Ile	Ala	Lys	Ala	Glu	Ser	Asn	Leu	Ser	Ile	Ala	Ser	Tyr
	290					295					300				
Asn	Lys	Ala	Val	Val	Glu	Ala	Val	Asn	Asp	Val	Ala	Arg	Ala	Ala	Ser
305					310					315					320
Gln	Val	Gln	Thr	Leu	Ala	Glu	Lys	Asn	Gln	His	Gln	Ala	Gln	Ile	Glu
				325					330					335	
Arg	Asp	Ala	Leu	Arg	Val	Val	Gly	Leu	Ala	Gln	Ala	Arg	Phe	Asn	Ala
			340					345					350		
Gly	Ile	Ile	Ala	Gly	Ser	Arg	Val	Ser	Glu	Ala	Arg	Ile	Pro	Ala	Leu
	355						360					365			
Arg	Glu	Arg	Ala	Asn	Gly	Leu	Leu	Leu	Gln	Gly	Gln	Trp	Leu	Asp	Ala
	370				375						380				
Ser	Ile	Gln	Leu	Thr	Gly	Ala	Leu	Gly	Gly	Gly	Tyr	Lys	Arg		
385					390					395					

<210> 305
 <211> 96
 <212> PRT
 <213> E. Coli

	<400>	305													
Met	Tyr	Cys	His	Ala	Lys	Leu	Lys	Asn	Ile	Ser	Gln	His	Thr	Val	Ile
1				5					10					15	
Ser	Ala	His	Leu	Phe	Leu	Pro	Asp	Tyr	Ser	Pro	Met	Asn	Arg	Asp	Ser
			20					25					30		
Phe	Tyr	Pro	Ala	Ile	Ala	Cys	Phe	Pro	Leu	Leu	Leu	Met	Leu	Ala	Gly
		35					40					45			
Cys	Ala	Pro	Met	His	Glu	Thr	Arg	Gln	Ala	Leu	Ser	Gln	Gln	Thr	Pro
	50					55					60				
Ala	Ala	Gln	Val	Asp	Thr	Ala	Leu	Pro	Thr	Ala	Leu	Lys	Met	Val	Gly
65				70					75						80
Gln	Thr	Ala	Asn	Gly	Gly	Trp	Ser	Ile	Thr	Ile	Ile	Asn	Ser	Leu	Pro
			85						90					95	

<210> 306
 <211> 315
 <212> PRT
 <213> E. Coli

	<400>	306													
Met	Arg	Val	Leu	Leu	Ala	Pro	Met	Glu	Gly	Val	Leu	Asp	Ser	Leu	Val
1			5						10					15	
Arg	Glu	Leu	Leu	Thr	Glu	Val	Asn	Asp	Tyr	Asp	Leu	Cys	Ile	Thr	Glu
		20						25					30		

Phe	Val	Arg	Val	Val	Asp	Gln	Leu	Leu	Pro	Val	Lys	Val	Phe	His	Arg
	35						40				45				
Ile	Cys	Pro	Glu	Leu	Gln	Asn	Ala	Ser	Arg	Thr	Pro	Ser	Gly	Thr	Leu
	50				55						60				
Val	Arg	Val	Gln	Leu	Leu	Gly	Gln	Phe	Pro	Gln	Trp	Leu	Ala	Glu	Asn
65				70					75					80	
Ala	Ala	Arg	Ala	Val	Glu	Leu	Gly	Ser	Trp	Gly	Val	Asp	Leu	Asn	Cys
			85					90						95	
Gly	Cys	Pro	Ser	Lys	Thr	Val	Asn	Gly	Ser	Gly	Gly	Gly	Ala	Thr	Leu
		100						105					110		
Leu	Lys	Asp	Pro	Glu	Leu	Ile	Tyr	Gln	Gly	Ala	Lys	Ala	Met	Arg	Glu
	115						120					125			
Ala	Val	Pro	Ala	His	Leu	Pro	Val	Ser	Val	Lys	Val	Arg	Leu	Gly	Trp
	130					135					140				
Asp	Ser	Gly	Glu	Lys	Lys	Phe	Glu	Ile	Ala	Asp	Ala	Val	Gln	Gln	Ala
145				150						155					160
Gly	Ala	Thr	Glu	Leu	Val	Val	His	Gly	Arg	Thr	Lys	Glu	Gln	Gly	Tyr
			165						170					175	
Arg	Ala	Glu	His	Ile	Asp	Trp	Gln	Ala	Ile	Gly	Asp	Ile	Arg	Gln	Arg
		180						185					190		
Leu	Asn	Ile	Pro	Val	Ile	Ala	Asn	Gly	Glu	Ile	Trp	Asp	Trp	Gln	Ser
	195						200					205			
Ala	Gln	Gln	Cys	Met	Ala	Ile	Ser	Gly	Cys	Asp	Ala	Val	Met	Ile	Gly
	210					215					220				
Arg	Gly	Ala	Leu	Asn	Ile	Pro	Asn	Leu	Ser	Arg	Val	Val	Lys	Tyr	Asn
225				230						235					240
Glu	Pro	Arg	Met	Pro	Trp	Pro	Glu	Val	Val	Ala	Leu	Leu	Gln	Lys	Tyr
			245					250						255	
Thr	Arg	Leu	Glu	Lys	Gln	Gly	Asp	Thr	Gly	Leu	Tyr	His	Val	Ala	Arg
		260						265					270		
Ile	Lys	Gln	Trp	Leu	Ser	Tyr	Leu	Arg	Lys	Glu	Tyr	Asp	Glu	Ala	Thr
	275						280					285			
Glu	Leu	Phe	Gln	His	Val	Arg	Val	Leu	Asn	Asn	Ser	Pro	Asp	Ile	Ala
	290					295					300				
Arg	Ala	Ile	Gln	Ala	Ile	Asp	Ile	Glu	Lys	Leu					
305					310					315					

<210> 307

<211> 296

<212> PRT

<213> E. Coli

<400> 307

Met	Thr	Ile	Ser	Thr	Thr	Ser	Thr	Pro	His	Asp	Ala	Val	Phe	Lys	Ser
1				5				10						15	
Phe	Leu	Arg	His	Pro	Asp	Thr	Ala	Arg	Asp	Phe	Ile	Asp	Ile	His	Leu
			20					25					30		
Pro	Ala	Pro	Leu	Arg	Lys	Leu	Cys	Asp	Leu	Thr	Thr	Leu	Lys	Leu	Glu
		35					40					45			
Pro	Asn	Ser	Phe	Ile	Asp	Glu	Asp	Leu	Arg	Gln	Tyr	Tyr	Ser	Asp	Leu
	50					55					60				
Leu	Trp	Ser	Val	Lys	Thr	Gln	Glu	Gly	Val	Gly	Tyr	Ile	Tyr	Val	Val
65				70					75					80	
Ile	Glu	His	Gln	Ser	Lys	Pro	Glu	Glu	Leu	Met	Ala	Phe	Arg	Met	Met
			85					90						95	
Arg	Tyr	Ser	Ile	Ala	Ala	Met	Gln	Asn	His	Leu	Asp	Ala	Gly	Tyr	Lys

Leu Asp Ala Glu Ser Val Ala Trp Leu Glu Arg Phe Leu His Asp Phe
 195 200 205
 Glu Gly Thr Val Val Ala Ile Thr His Asp Arg Tyr Phe Leu Asp Asn
 210 215 220
 Val Ala Gly Trp Ile Leu Glu Leu Asp Arg Gly Glu Gly Ile Pro Trp
 225 230 235 240
 Glu Gly Asn Tyr Ser Ser Trp Leu Glu Gln Lys Asp Gln Arg Leu Ala
 245 250 255
 Gln Glu Ala Ser Gln Glu Ala Ala Arg Arg Lys Ser Ile Glu Lys Glu
 260 265 270
 Leu Glu Trp Val Arg Gln Gly Thr Lys Gly Arg Gln Ser Lys Gly Lys
 275 280 285
 Ala Arg Leu Ala Arg Phe Glu Glu Leu Asn Ser Thr Glu Tyr Gln Lys
 290 295 300
 Arg Asn Glu Thr Asn Glu Leu Phe Ile Pro Pro Gly Pro Arg Leu Gly
 305 310 315 320
 Asp Lys Val Leu Glu Val Ser Asn Leu Arg Lys Ser Tyr Gly Asp Arg
 325 330 335
 Leu Leu Ile Asp Asp Leu Ser Phe Ser Ile Pro Lys Gly Ala Ile Val
 340 345 350
 Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Phe Arg Met
 355 360 365
 Ile Ser Gly Gln Glu Gln Pro Asp Ser Gly Thr Ile Thr Leu Gly Glu
 370 375 380
 Thr Val Lys Leu Ala Ser Val Asp Gln Phe Arg Asp Ser Met Asp Asn
 385 390 395 400
 Ser Lys Thr Val Trp Glu Glu Val Ser Gly Gly Leu Asp Ile Met Lys
 405 410 415
 Ile Gly Asn Thr Glu Met Pro Ser Arg Ala Tyr Val Gly Arg Phe Asn
 420 425 430
 Phe Lys Gly Val Asp Gln Gly Lys Arg Val Gly Glu Leu Ser Gly Gly
 435 440 445
 Glu Arg Gly Arg Leu His Leu Ala Lys Leu Leu Gln Val Gly Gly Asn
 450 455 460
 Met Leu Leu Leu Asp Glu Pro Thr Asn Asp Leu Asp Ile Glu Thr Leu
 465 470 475 480
 Arg Ala Leu Glu Asn Ala Leu Leu Glu Phe Pro Gly Cys Ala Met Val
 485 490 495
 Ile Ser His Asp Arg Trp Phe Leu Asp Arg Ile Ala Thr His Ile Leu
 500 505 510
 Asp Tyr Gln Asp Glu Gly Lys Val Glu Phe Phe Glu Gly Asn Phe Thr
 515 520 525
 Glu Tyr Glu Glu Tyr Lys Lys Arg Thr Leu Gly Ala Asp Ala Leu Glu
 530 535 540
 Pro Lys Arg Ile Lys Tyr Lys Arg Ile Ala Lys
 545 550 555

<210> 309
 <211> 173
 <212> PRT
 <213> E. Coli

<400> 309
 Met Ser Lys Pro Lys Tyr Pro Phe Glu Lys Arg Leu Glu Val Val Asn
 1 5 10 15

His Tyr Phe Thr Thr Asp Asp Gly Tyr Arg Ile Ile Ser Ala Arg Phe
 20 25 30
 Gly Val Pro Arg Thr Gln Val Arg Thr Trp Val Ala Leu Tyr Glu Lys
 35 40 45
 His Gly Glu Lys Gly Leu Ile Pro Lys Pro Lys Gly Val Ser Ala Asp
 50 55 60
 Pro Glu Leu Arg Ile Lys Val Val Lys Ala Val Ile Glu Gln His Met
 65 70 75 80
 Ser Leu Asn Gln Ala Ala Ala His Phe Met Leu Ala Gly Ser Gly Ser
 85 90 95
 Val Ala Arg Trp Leu Lys Val Tyr Glu Glu Arg Gly Glu Ala Gly Leu
 100 105 110
 Arg Ala Leu Lys Ile Gly Thr Lys Arg Asn Ile Ala Ile Ser Val Asp
 115 120 125
 Pro Glu Lys Ala Ala Ser Ala Leu Glu Leu Ser Lys Asp Arg Arg Ile
 130 135 140
 Glu Asp Leu Glu Arg Gln Val Arg Phe Leu Glu Thr Arg Leu Met Tyr
 145 150 155 160
 Leu Lys Lys Leu Lys Ala Leu Ala His Pro Thr Lys Lys
 165 170

<210> 310

<211> 283

<212> PRT

<213> E. Coli

<400> 310

Met Lys Val Leu Asn Glu Leu Arg Gln Phe Tyr Pro Leu Asp Glu Leu
 1 5 10 15
 Leu Arg Ala Ala Glu Ile Pro Arg Ser Thr Phe Tyr Tyr His Leu Lys
 20 25 30
 Ala Leu Ser Lys Pro Asp Lys Tyr Ala Asp Val Lys Lys Arg Ile Ser
 35 40 45
 Glu Ile Tyr His Glu Asn Arg Gly Arg Tyr Gly Tyr Arg Arg Val Thr
 50 55 60
 Leu Ser Leu His Arg Glu Gly Lys Gln Ile Asn His Lys Ala Val Gln
 65 70 75 80
 Arg Leu Met Gly Thr Leu Ser Leu Lys Ala Ala Ile Lys Val Lys Arg
 85 90 95
 Tyr Arg Ser Tyr Arg Gly Glu Val Gly Gln Thr Ala Pro Asn Val Leu
 100 105 110
 Gln Arg Asp Phe Lys Ala Thr Arg Pro Asn Glu Lys Trp Val Thr Asp
 115 120 125
 Val Thr Glu Phe Ala Val Asn Gly Arg Lys Leu Tyr Leu Ser Pro Val
 130 135 140
 Ile Asp Leu Phe Asn Asn Glu Val Ile Ser Tyr Ser Leu Ser Glu Arg
 145 150 155 160
 Pro Val Met Asn Met Val Glu Asn Met Leu Asp Gln Ala Phe Lys Lys
 165 170 175
 Leu Asn Pro His Glu His Pro Val Leu His Ser Asp Gln Gly Trp Gln
 180 185 190
 Tyr Arg Met Arg Arg Tyr Gln Asn Ile Leu Lys Glu His Gly Ile Lys
 195 200 205
 Gln Ser Met Ser Arg Lys Gly Asn Cys Leu Asp Asn Ala Val Val Glu
 210 215 220
 Cys Phe Phe Gly Thr Leu Lys Ser Glu Cys Phe Tyr Leu Asp Glu Phe

225 230 235 240
 Ser Asn Ile Ser Glu Leu Lys Asp Ala Val Thr Glu Tyr Ile Glu Tyr
 245 250 255
 Tyr Asn Ser Arg Arg Ile Ser Leu Lys Leu Lys Gly Leu Thr Pro Ile
 260 265 270
 Glu Tyr Arg Asn Gln Thr Tyr Met Pro Arg Val
 275 280

<210> 311
 <211> 38
 <212> PRT
 <213> E. Coli

<400> 311
 Met Lys Val Arg Ala Ser Val Lys Lys Leu Cys Arg Asn Cys Lys Ile
 1 5 10 15
 Val Lys Arg Asp Gly Val Ile Arg Val Ile Cys Ser Ala Glu Pro Lys
 20 25 30
 His Lys Gln Arg Gln Gly
 35

<210> 312
 <211> 443
 <212> PRT
 <213> E. Coli

<400> 312
 Met Ala Lys Gln Pro Gly Leu Asp Phe Gln Ser Ala Lys Gly Gly Leu
 1 5 10 15
 Gly Glu Leu Lys Arg Arg Leu Leu Phe Val Ile Gly Ala Leu Ile Val
 20 25 30
 Phe Arg Ile Gly Ser Phe Ile Pro Ile Pro Gly Ile Asp Ala Ala Val
 35 40 45
 Leu Ala Lys Leu Leu Glu Gln Gln Arg Gly Thr Ile Ile Glu Met Phe
 50 55 60
 Asn Met Phe Ser Gly Gly Ala Leu Ser Arg Ala Ser Ile Phe Ala Leu
 65 70 75 80
 Gly Ile Met Pro Tyr Ile Ser Ala Ser Ile Ile Ile Gln Leu Leu Thr
 85 90 95
 Val Val His Pro Thr Leu Ala Glu Ile Lys Lys Glu Gly Glu Ser Gly
 100 105 110
 Arg Arg Lys Ile Ser Gln Tyr Thr Arg Tyr Gly Thr Leu Val Leu Ala
 115 120 125
 Ile Phe Gln Ser Ile Gly Ile Ala Thr Gly Leu Pro Asn Met Pro Gly
 130 135 140
 Met Gln Gly Leu Val Ile Asn Pro Gly Phe Ala Phe Tyr Phe Thr Ala
 145 150 155 160
 Val Val Ser Leu Val Thr Gly Thr Met Phe Leu Met Trp Leu Gly Glu
 165 170 175
 Gln Ile Thr Glu Arg Gly Ile Gly Asn Gly Ile Ser Ile Ile Ile Phe
 180 185 190
 Ala Gly Ile Val Ala Gly Leu Pro Pro Ala Ile Ala His Thr Ile Glu
 195 200 205
 Gln Ala Arg Gln Gly Asp Leu His Phe Leu Val Leu Leu Val Ala
 210 215 220
 Val Leu Val Phe Ala Val Thr Phe Phe Val Val Phe Val Glu Arg Gly

225		230		235		240
Gln Arg Arg Ile Val	Val Asn Tyr Ala Lys Arg Gln Gln Gly Arg Arg					
	245		250		255	
Val Tyr Ala Ala Gln Ser Thr His Leu Pro Leu Lys Val Asn Met Ala						
	260		265		270	
Gly Val Ile Pro Ala Ile Phe Ala Ser Ser Ile Ile Leu Phe Pro Ala						
	275		280		285	
Thr Ile Ala Ser Trp Phe Gly Gly Thr Gly Trp Asn Trp Leu Thr						
	290		295		300	
Thr Ile Ser Leu Tyr Leu Gln Pro Gly Gln Pro Leu Tyr Val Leu Leu						
305		310		315		320
Tyr Ala Ser Ala Ile Ile Phe Phe Cys Phe Phe Tyr Thr Ala Leu Val						
	325		330		335	
Phe Asn Pro Arg Glu Thr Ala Asp Asn Leu Lys Lys Ser Gly Ala Phe						
	340		345		350	
Val Pro Gly Ile Arg Pro Gly Glu Gln Thr Ala Lys Tyr Ile Asp Lys						
	355		360		365	
Val Met Thr Arg Leu Thr Leu Val Gly Ala Leu Tyr Ile Thr Phe Ile						
	370		375		380	
Cys Leu Ile Pro Glu Phe Met Arg Asp Ala Met Lys Val Pro Phe Tyr						
385		390		395		400
Phe Gly Gly Thr Ser Leu Leu Ile Val Val Val Val Ile Met Asp Phe						
	405		410		415	
Met Ala Gln Val Gln Thr Leu Met Met Ser Ser Gln Tyr Glu Ser Ala						
	420		425		430	
Leu Lys Lys Ala Asn Leu Lys Gly Tyr Gly Arg						
	435		440			

<210> 313

<211> 144

<212> PRT

<213> E. Coli

<400> 313

Met Arg Leu Asn Thr Leu Ser Pro Ala Glu Gly Ser Lys Lys Ala Gly	
1	5 10 15
Lys Arg Leu Gly Arg Gly Ile Gly Ser Gly Leu Gly Lys Thr Gly Gly	
	20 25 30
Arg Gly His Lys Gly Gln Lys Ser Arg Ser Gly Gly Val Arg Arg	
	35 40 45
Gly Phe Glu Gly Gly Gln Met Pro Leu Tyr Arg Arg Leu Pro Lys Phe	
	50 55 60
Gly Phe Thr Ser Arg Lys Ala Ala Ile Thr Ala Glu Ile Arg Leu Ser	
65	70 75 80
Asp Leu Ala Lys Val Glu Gly Gly Val Val Asp Leu Asn Thr Leu Lys	
	85 90 95
Ala Ala Asn Ile Ile Gly Ile Gln Ile Glu Phe Ala Lys Val Ile Leu	
	100 105 110
Ala Gly Glu Val Thr Thr Pro Val Thr Val Arg Gly Leu Arg Val Thr	
	115 120 125
Lys Gly Ala Arg Ala Ala Ile Glu Ala Ala Gly Gly Lys Ile Glu Glu	
	130 135 140

<210> 314

<211> 59
 <212> PRT
 <213> E. Coli

<400> 314
 Met Ala Lys Thr Ile Lys Ile Thr Gln Thr Arg Ser Ala Ile Gly Arg
 1 5 10 15
 Leu Pro Lys His Lys Ala Thr Leu Leu Gly Leu Gly Leu Arg Arg Ile
 20 25 30
 Gly His Thr Val Glu Arg Glu Asp Thr Pro Ala Ile Arg Gly Met Ile
 35 40 45
 Asn Ala Val Ser Phe Met Val Lys Val Glu Glu
 50 55

<210> 315
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 315
 Met Ala His Ile Glu Lys Gln Ala Gly Glu Leu Gln Glu Lys Leu Ile
 1 5 10 15
 Ala Val Asn Arg Val Ser Lys Thr Val Lys Gly Gly Arg Ile Phe Ser
 20 25 30
 Phe Thr Ala Leu Thr Val Val Gly Asp Gly Asn Gly Arg Val Gly Phe
 35 40 45
 Gly Tyr Gly Lys Ala Arg Glu Val Pro Ala Ala Ile Gln Lys Ala Met
 50 55 60
 Glu Lys Ala Arg Arg Asn Met Ile Asn Val Ala Leu Asn Asn Gly Thr
 65 70 75 80
 Leu Gln His Pro Val Lys Gly Val His Thr Gly Ser Arg Val Phe Met
 85 90 95
 Gln Pro Ala Ser Glu Gly Thr Gly Ile Ile Ala Gly Gly Ala Met Arg
 100 105 110
 Ala Val Leu Glu Val Ala Gly Val His Asn Val Leu Ala Lys Ala Tyr
 115 120 125
 Gly Ser Thr Asn Pro Ile Asn Val Val Arg Ala Thr Ile Asp Gly Leu
 130 135 140
 Glu Asn Met Asn Ser Pro Glu Met Val Ala Ala Lys Arg Gly Lys Ser
 145 150 155 160
 Val Glu Glu Ile Leu Gly Lys
 165

<210> 316
 <211> 117
 <212> PRT
 <213> E. Coli

<400> 316
 Met Asp Lys Lys Ser Ala Arg Ile Arg Arg Ala Thr Arg Ala Arg Arg
 1 5 10 15
 Lys Leu Gln Glu Leu Gly Ala Thr Arg Leu Val Val His Arg Thr Pro
 20 25 30
 Arg His Ile Tyr Ala Gln Val Ile Ala Pro Asn Gly Ser Glu Val Leu

	35					40					45								
Val	Ala	Ala	Ser	Thr	Val	Glu	Lys	Ala	Ile	Ala	Glu	Gln	Leu	Lys	Tyr				
	50					55					60								
Thr	Gly	Asn	Lys	Asp	Ala	Ala	Ala	Ala	Val	Gly	Lys	Ala	Val	Ala	Glu				
65					70					75					80				
Arg	Ala	Leu	Glu	Lys	Gly	Ile	Lys	Asp	Val	Ser	Phe	Asp	Arg	Ser	Gly				
				85					90					95					
Phe	Gln	Tyr	His	Gly	Arg	Val	Gln	Ala	Leu	Ala	Asp	Ala	Ala	Arg	Glu				
			100					105					110						
Ala	Gly	Leu	Gln	Phe															
			115																

<210> 317
 <211> 177
 <212> PRT
 <213> E. Coli

Met	Ser	Arg	Val	Ala	Lys	Ala	Pro	Val	Val	Val	Pro	Ala	Gly	Val	Asp				
1				5					10					15					
Val	Lys	Ile	Asn	Gly	Gln	Val	Ile	Thr	Ile	Lys	Gly	Lys	Asn	Gly	Glu				
			20					25					30						
Leu	Thr	Arg	Thr	Leu	Asn	Asp	Ala	Val	Glu	Val	Lys	His	Ala	Asp	Asn				
		35					40					45							
Thr	Leu	Thr	Phe	Gly	Pro	Arg	Asp	Gly	Tyr	Ala	Asp	Gly	Trp	Ala	Gln				
	50					55					60								
Ala	Gly	Thr	Ala	Arg	Ala	Leu	Leu	Asn	Ser	Met	Val	Ile	Gly	Val	Thr				
65					70					75					80				
Glu	Gly	Phe	Thr	Lys	Lys	Leu	Gln	Leu	Val	Gly	Val	Gly	Tyr	Arg	Ala				
				85					90					95					
Ala	Val	Lys	Gly	Asn	Val	Ile	Asn	Leu	Ser	Leu	Gly	Phe	Ser	His	Pro				
			100					105					110						
Val	Asp	His	Gln	Leu	Pro	Ala	Gly	Ile	Thr	Ala	Glu	Cys	Pro	Thr	Gln				
		115					120					125							
Thr	Glu	Ile	Val	Leu	Lys	Gly	Ala	Asp	Lys	Gln	Val	Ile	Gly	Gln	Val				
	130					135					140								
Ala	Ala	Asp	Leu	Arg	Ala	Tyr	Arg	Arg	Pro	Glu	Pro	Tyr	Lys	Gly	Lys				
145					150					155					160				
Gly	Val	Arg	Tyr	Ala	Asp	Glu	Val	Val	Arg	Thr	Lys	Glu	Ala	Lys	Lys				
				165					170					175					

Lys

<210> 318
 <211> 130
 <212> PRT
 <213> E. Coli

Met	Ser	Met	Gln	Asp	Pro	Ile	Ala	Asp	Met	Leu	Thr	Arg	Ile	Arg	Asn				
1				5					10					15					
Gly	Gln	Ala	Ala	Asn	Lys	Ala	Ala	Val	Thr	Met	Pro	Ser	Ser	Lys	Leu				
			20					25					30						
Lys	Val	Ala	Ile	Ala	Asn	Val	Leu	Lys	Glu	Glu	Gly	Phe	Ile	Glu	Asp				
		35					40					45							

Phe Lys Val Glu Gly Asp Thr Lys Pro Glu Leu Glu Leu Thr Leu Lys
 50 55 60
 Tyr Phe Gln Gly Lys Ala Val Val Glu Ser Ile Gln Arg Val Ser Arg
 65 70 75 80
 Pro Gly Leu Arg Ile Tyr Lys Arg Lys Asp Glu Leu Pro Lys Val Met
 85 90 95
 Ala Gly Leu Gly Ile Ala Val Val Ser Thr Ser Lys Gly Val Met Thr
 100 105 110
 Asp Arg Ala Ala Arg Gln Ala Gly Leu Gly Gly Glu Ile Ile Cys Tyr
 115 120 125
 Val Ala
 130

<210> 319
 <211> 101
 <212> PRT
 <213> E. Coli

<400> 319
 Met Ala Lys Gln Ser Met Lys Ala Arg Glu Val Lys Arg Val Ala Leu
 1 5 10 15
 Ala Asp Lys Tyr Phe Ala Lys Arg Ala Glu Leu Lys Ala Ile Ile Ser
 20 25 30
 Asp Val Asn Ala Ser Asp Glu Asp Arg Trp Asn Ala Val Leu Lys Leu
 35 40 45
 Gln Thr Leu Pro Arg Asp Ser Ser Pro Ser Arg Gln Arg Asn Arg Cys
 50 55 60
 Arg Gln Thr Gly Arg Pro His Gly Phe Leu Arg Lys Phe Gly Leu Ser
 65 70 75 80
 Arg Ile Lys Val Arg Glu Ala Ala Met Arg Gly Glu Ile Pro Gly Leu
 85 90 95
 Lys Lys Ala Ser Trp
 100

<210> 320
 <211> 179
 <212> PRT
 <213> E. Coli

<400> 320
 Met Ala Lys Leu His Asp Tyr Tyr Lys Asp Glu Val Val Lys Lys Leu
 1 5 10 15
 Met Thr Glu Phe Asn Tyr Asn Ser Val Met Gln Val Pro Arg Val Glu
 20 25 30
 Lys Ile Thr Leu Asn Met Gly Val Gly Glu Ala Ile Ala Asp Lys Lys
 35 40 45
 Leu Leu Asp Asn Ala Ala Ala Asp Leu Ala Ala Ile Ser Gly Gln Lys
 50 55 60
 Pro Leu Ile Thr Lys Ala Arg Lys Ser Val Ala Gly Phe Lys Ile Arg
 65 70 75 80
 Gln Gly Tyr Pro Ile Gly Cys Lys Val Thr Leu Arg Gly Glu Arg Met
 85 90 95
 Trp Glu Phe Phe Glu Arg Leu Ile Thr Ile Ala Val Pro Arg Ile Arg
 100 105 110

Asp	Phe	Arg	Gly	Leu	Ser	Ala	Lys	Ser	Phe	Asp	Gly	Arg	Gly	Asn	Tyr
	115						120					125			
Ser	Met	Gly	Val	Arg	Glu	Gln	Ile	Ile	Phe	Pro	Glu	Ile	Asp	Tyr	Asp
	130					135					140				
Lys	Val	Asp	Arg	Val	Arg	Gly	Leu	Asp	Ile	Thr	Ile	Thr	Thr	Thr	Ala
145					150					155					160
Lys	Ser	Asp	Glu	Glu	Gly	Arg	Ala	Leu	Leu	Ala	Ala	Phe	Asp	Phe	Pro
			165					170						175	
Phe	Arg	Lys													

<210> 321Z
 <211> 104
 <212> PRT
 <213> E. Coli

<400> 321

Met	Ala	Ala	Lys	Ile	Arg	Arg	Asp	Asp	Glu	Val	Ile	Val	Leu	Thr	Gly
1			5						10				15		
Lys	Asp	Lys	Gly	Lys	Arg	Gly	Lys	Val	Lys	Asn	Val	Leu	Ser	Ser	Gly
		20					25					30			
Lys	Val	Ile	Val	Glu	Gly	Ile	Asn	Leu	Val	Lys	Lys	His	Gln	Lys	Pro
	35					40						45			
Val	Pro	Ala	Leu	Asn	Gln	Pro	Gly	Gly	Ile	Val	Glu	Lys	Glu	Ala	Ala
50					55						60				
Ile	Gln	Val	Ser	Asn	Val	Ala	Ile	Phe	Asn	Ala	Ala	Thr	Gly	Lys	Ala
65				70					75						80
Asp	Arg	Val	Gly	Phe	Arg	Phe	Glu	Asp	Gly	Lys	Lys	Val	Arg	Phe	Phe
			85					90						95	
Lys	Ser	Asn	Ser	Glu	Thr	Ile	Lys								
			100												

<210> 322
 <211> 123
 <212> PRT
 <213> E. Coli

<400> 322

Met	Ile	Gln	Glu	Gln	Thr	Met	Leu	Asn	Val	Ala	Asp	Asn	Ser	Gly	Ala
1				5					10					15	
Arg	Arg	Val	Met	Cys	Ile	Lys	Val	Leu	Gly	Gly	Ser	His	Arg	Arg	Tyr
		20						25					30		
Ala	Gly	Val	Gly	Asp	Ile	Ile	Lys	Ile	Thr	Ile	Lys	Glu	Ala	Ile	Pro
	35					40						45			
Arg	Gly	Lys	Val	Lys	Lys	Gly	Asp	Val	Leu	Lys	Ala	Val	Val	Val	Arg
50					55						60				
Thr	Lys	Lys	Gly	Val	Arg	Arg	Pro	Asp	Gly	Ser	Val	Ile	Arg	Phe	Asp
65				70					75						80
Gly	Asn	Ala	Cys	Val	Leu	Leu	Asn	Asn	Asn	Ser	Glu	Gln	Pro	Ile	Gly
			85					90						95	
Thr	Arg	Ile	Phe	Gly	Pro	Val	Thr	Arg	Glu	Leu	Arg	Ser	Glu	Lys	Phe
			100				105						110		
Met	Lys	Ile	Ile	Ser	Leu	Ala	Pro	Glu	Val	Leu					
	115						120								

<210> 323
 <211> 188
 <212> PRT
 <213> E. Coli

<400> 323

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Met Phe Lys Gly Gln Lys Thr Leu Ala Ala Leu Ala Val Ser Leu Leu
 1           5           10           15
Phe Thr Ala Pro Val Tyr Ala Ala Asp Glu Gly Ser Gly Glu Ile His
      20           25           30
Phe Lys Gly Glu Val Ile Glu Ala Pro Cys Glu Ile His Pro Glu Asp
      35           40           45
Ile Asp Lys Asn Ile Asp Leu Gly Gln Val Thr Thr Thr His Ile Asn
      50           55           60
Arg Glu His His Ser Asn Lys Val Ala Val Asp Ile Arg Leu Ile Asn
      65           70           75           80
Cys Asp Leu Pro Ala Ser Asp Asn Gly Ser Gly Met Pro Val Ser Lys
      85           90           95
Val Gly Val Thr Phe Asp Ser Thr Ala Lys Thr Thr Gly Ala Thr Pro
      100           105           110
Leu Leu Ser Asn Thr Ser Ala Gly Glu Ala Thr Gly Val Gly Val Arg
      115           120           125
Leu Met Asp Lys Asn Asp Gly Asn Ile Val Leu Gly Ser Ala Ala Pro
      130           135           140
Asp Leu Asp Leu Asp Ala Ser Ser Ser Glu Gln Thr Leu Asn Phe Phe
      145           150           155           160
Ala Trp Met Glu Gln Ile Asp Asn Ala Val Asp Val Thr Ala Gly Glu
      165           170           175
Val Thr Ala Asn Ala Thr Tyr Val Leu Asp Tyr Lys
      180           185

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<210> 324
 <211> 427
 <212> PRT
 <213> E. Coli

<400> 324

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Met Ala Asp Thr Lys Ala Lys Leu Thr Leu Asn Gly Asp Thr Ala Val
 1           5           10           15
Glu Leu Asp Val Leu Lys Gly Thr Leu Gly Gln Asp Val Ile Asp Ile
      20           25           30
Arg Thr Leu Gly Ser Lys Gly Val Phe Thr Phe Asp Pro Gly Phe Thr
      35           40           45
Ser Thr Ala Ser Cys Glu Ser Lys Ile Thr Phe Ile Asp Gly Asp Glu
      50           55           60
Gly Ile Leu Leu His Arg Gly Phe Pro Ile Asp Gln Leu Ala Thr Asp
      65           70           75           80
Ser Asn Tyr Leu Glu Val Cys Tyr Ile Leu Leu Asn Gly Glu Lys Pro
      85           90           95
Thr Gln Glu Gln Tyr Asp Glu Phe Lys Thr Thr Val Thr Arg His Thr
      100           105           110
Met Ile His Glu Gln Ile Thr Arg Leu Phe His Ala Phe Arg Arg Asp
      115           120           125
Ser His Pro Met Ala Val Met Cys Gly Ile Thr Gly Ala Leu Ala Ala
      130           135           140

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Phe	Tyr	His	Asp	Ser	Leu	Asp	Val	Asn	Asn	Pro	Arg	His	Arg	Glu	Ile
145					150					155					160
Ala	Ala	Phe	Arg	Leu	Leu	Ser	Lys	Met	Pro	Thr	Met	Ala	Ala	Met	Cys
				165					170					175	
Tyr	Lys	Tyr	Ser	Ile	Gly	Gln	Pro	Phe	Val	Tyr	Pro	Arg	Asn	Asp	Leu
			180					185					190		
Ser	Tyr	Ala	Gly	Asn	Phe	Leu	Asn	Met	Met	Phe	Ser	Thr	Pro	Cys	Glu
		195					200					205			
Pro	Tyr	Glu	Val	Asn	Pro	Ile	Leu	Glu	Arg	Ala	Met	Asp	Arg	Ile	Leu
	210					215					220				
Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Ala	Ser	Thr	Ser	Thr	Val	Arg
225					230					235					240
Thr	Ala	Gly	Ser	Ser	Gly	Ala	Asn	Pro	Phe	Ala	Cys	Ile	Ala	Ala	Gly
				245					250					255	
Ile	Ala	Ser	Leu	Trp	Gly	Pro	Ala	His	Gly	Gly	Ala	Asn	Glu	Ala	Ala
			260					265					270		
Leu	Lys	Met	Leu	Glu	Glu	Ile	Ser	Ser	Val	Lys	His	Ile	Pro	Glu	Phe
		275					280					285			
Val	Arg	Arg	Ala	Lys	Asp	Lys	Asn	Asp	Ser	Phe	Arg	Leu	Met	Gly	Phe
	290					295					300				
Gly	His	Arg	Val	Tyr	Lys	Asn	Tyr	Asp	Pro	Arg	Ala	Thr	Val	Met	Arg
305					310					315					320
Glu	Thr	Cys	His	Glu	Val	Leu	Lys	Glu	Leu	Gly	Thr	Lys	Asp	Asp	Leu
				325					330					335	
Leu	Glu	Val	Ala	Met	Glu	Leu	Glu	Asn	Ile	Ala	Leu	Asn	Asp	Pro	Tyr
			340					345					350		
Phe	Ile	Glu	Lys	Lys	Leu	Tyr	Pro	Asn	Val	Asp	Phe	Tyr	Ser	Gly	Ile
		355					360					365			
Ile	Leu	Lys	Ala	Met	Gly	Ile	Pro	Ser	Ser	Met	Phe	Thr	Val	Ile	Phe
	370					375					380				
Ala	Met	Ala	Arg	Thr	Val	Gly	Trp	Ile	Ala	His	Trp	Ser	Glu	Met	His
385					390					395					400
Ser	Asp	Gly	Met	Lys	Ile	Ala	Arg	Pro	Arg	Gln	Leu	Tyr	Thr	Gly	Tyr
				405					410					415	
Glu	Lys	Arg	Asp	Phe	Lys	Ser	Asp	Ile	Lys	Arg					
			420					425							

<210> 325

<211> 477

<212> PRT

<213> E. Coli

<400> 325

Met	Lys	Val	Thr	Leu	Pro	Glu	Phe	Glu	Arg	Ala	Gly	Val	Met	Val	Val
1				5				10					15		
Gly	Asp	Val	Met	Leu	Asp	Arg	Tyr	Trp	Tyr	Gly	Pro	Thr	Ser	Arg	Ile
			20					25					30		
Ser	Pro	Glu	Ala	Pro	Val	Pro	Val	Val	Lys	Val	Asn	Thr	Ile	Glu	Glu
		35				40						45			
Arg	Pro	Gly	Gly	Ala	Ala	Asn	Val	Ala	Met	Asn	Ile	Ala	Ser	Leu	Gly
	50					55					60				
Ala	Asn	Ala	Arg	Leu	Val	Gly	Leu	Thr	Gly	Ile	Asp	Asp	Ala	Ala	Arg
65					70					75					80
Ala	Leu	Ser	Lys	Ser	Leu	Ala	Asp	Val	Asn	Val	Lys	Cys	Asp	Phe	Val
				85					90					95	
Ser	Val	Pro	Thr	His	Pro	Thr	Ile	Thr	Lys	Leu	Arg	Val	Leu	Ser	Arg

Glu	Arg	Leu	Pro	Glu	Pro	Leu	Ala	Glu	Glu	Ser	Leu	Ser	Ala	Gln	Ala		
			20					25					30				
Lys	Ser	Val	Leu	Thr	Phe	Ser	Asp	Phe	Val	Gln	Asp	Ser	Val	Ile	Ala		
		35					40					45					
His	Pro	Glu	Trp	Leu	Thr	Glu	Leu	Glu	Ser	Gln	Pro	Pro	Gln	Ala	Asp		
	50					55					60						
Glu	Trp	Gln	His	Tyr	Ala	Ala	Trp	Leu	Gln	Glu	Ala	Leu	Cys	Asn	Val		
65				70					75					80			
Ser	Asp	Glu	Ala	Gly	Leu	Met	Arg	Glu	Leu	Arg	Leu	Phe	Arg	Arg	Arg		
				85				90						95			
Ile	Met	Val	Arg	Ile	Ala	Trp	Ala	Gln	Thr	Leu	Ala	Leu	Val	Thr	Glu		
		100						105					110				
Glu	Ser	Ile	Leu	Gln	Gln	Leu	Ser	Tyr	Leu	Ala	Glu	Thr	Leu	Ile	Val		
		115					120					125					
Ala	Ala	Arg	Asp	Trp	Leu	Tyr	Asp	Ala	Cys	Cys	Arg	Glu	Trp	Gly	Thr		
	130					135					140						
Pro	Cys	Asn	Ala	Gln	Gly	Glu	Ala	Gln	Pro	Leu	Leu	Ile	Leu	Gly	Met		
145					150					155					160		
Gly	Lys	Leu	Gly	Gly	Gly	Glu	Leu	Asn	Phe	Ser	Ser	Asp	Ile	Asp	Leu		
			165					170						175			
Ile	Phe	Ala	Trp	Pro	Glu	His	Gly	Cys	Thr	Gln	Gly	Gly	Arg	Arg	Glu		
		180					185						190				
Leu	Asp	Asn	Ala	Gln	Phe	Phe	Thr	Arg	Met	Gly	Gln	Arg	Leu	Ile	Lys		
		195					200					205					
Val	Leu	Asp	Gln	Pro	Thr	Gln	Asp	Gly	Phe	Val	Tyr	Arg	Val	Asp	Met		
	210					215					220						
Arg	Leu	Arg	Pro	Phe	Gly	Glu	Ser	Gly	Pro	Leu	Val	Leu	Ser	Phe	Ala		
225					230					235					240		
Ala	Leu	Glu	Asp	Tyr	Tyr	Gln	Glu	Gln	Gly	Arg	Asp	Trp	Glu	Arg	Tyr		
			245						250					255			
Ala	Met	Val	Lys	Ala	Arg	Ile	Met	Gly	Asp	Ser	Glu	Gly	Val	Tyr	Ala		
		260						265					270				
Asn	Glu	Leu	Arg	Ala	Met	Leu	Arg	Pro	Phe	Val	Phe	Arg	Arg	Tyr	Ile		
	275					280						285					
Asp	Phe	Ser	Val	Ile	Gln	Ser	Leu	Arg	Asn	Met	Lys	Gly	Met	Ile	Ala		
	290					295					300						
Arg	Glu	Val	Arg	Arg	Arg	Gly	Leu	Thr	Asp	Asn	Ile	Lys	Leu	Gly	Ala		
305					310					315					320		
Gly	Gly	Ile	Arg	Glu	Ile	Glu	Phe	Ile	Val	Gln	Val	Phe	Gln	Leu	Ile		
			325						330					335			
Arg	Gly	Gly	Arg	Glu	Pro	Ser	Leu	Gln	Ser	Arg	Ser	Leu	Leu	Pro	Thr		
			340					345						350			
Leu	Ser	Ala	Ile	Ala	Glu	Leu	His	Leu	Leu	Ser	Glu	Asn	Asp	Ala	Glu		
		355					360					365					
Gln	Leu	Arg	Val	Ala	Tyr	Leu	Phe	Leu	Arg	Arg	Leu	Glu	Asn	Leu	Leu		
	370					375					380						
Gln	Ser	Ile	Asn	Asp	Glu	Gln	Thr	Gln	Thr	Leu	Pro	Ser	Asp	Glu	Leu		
385				390						395					400		
Asn	Arg	Ala	Arg	Leu	Ala	Trp	Ala	Met	Asp	Phe	Ala	Asp	Trp	Pro	Gln		
			405						410					415			
Leu	Thr	Gly	Ala	Leu	Thr	Ala	His	Met	Thr	Asn	Val	Arg	Arg	Val	Phe		
		420						425					430				
Asn	Glu	Leu	Ile	Gly	Asp	Asp	Glu	Ser	Glu	Thr	Gln	Glu	Glu	Ser	Leu		
	435					440					445						
Ser	Glu	Gln	Trp	Arg	Glu	Leu	Trp	Gln	Asp	Ala	Leu	Gln	Glu	Asp	Asp		
	450					455					460						
Thr	Thr	Pro	Val	Leu	Ala	His	Leu	Ser	Glu	Asp	Asp	Arg	Lys	Gln	Val		

465					470					475					480
Leu	Thr	Leu	Ile	Ala	Asp	Phe	Arg	Lys	Glu	Leu	Asp	Lys	Arg	Thr	Ile
				485					490						495
Gly	Pro	Arg	Gly	Arg	Gln	Val	Leu	Asp	His	Leu	Met	Pro	His	Leu	Leu
			500					505					510		
Ser	Asp	Val	Cys	Ala	Arg	Glu	Asp	Ala	Ala	Val	Thr	Leu	Ser	Arg	Ile
		515					520					525			
Thr	Ala	Leu	Leu	Val	Gly	Ile	Val	Thr	Arg	Thr	Thr	Tyr	Leu	Glu	Leu
	530					535					540				
Leu	Ser	Glu	Phe	Pro	Ala	Ala	Leu	Lys	His	Leu	Ile	Ser	Leu	Cys	Ala
545					550					555					560
Ala	Ser	Pro	Met	Ile	Ala	Ser	Gln	Leu	Ala	Arg	Tyr	Pro	Leu	Leu	Leu
				565					570						575
Asp	Glu	Leu	Leu	Asp	Pro	Asn	Thr	Leu	Tyr	Gln	Pro	Thr	Ala	Thr	Asp
		580						585					590		
Ala	Tyr	Arg	Asp	Glu	Leu	Arg	Gln	Tyr	Leu	Leu	Arg	Val	Pro	Glu	Asp
		595					600					605			
Asp	Glu	Glu	Gln	Gln	Leu	Glu	Ala	Leu	Arg	Gln	Phe	Lys	Gln	Ala	Gln
610						615					620				
Leu	Leu	Arg	Ile	Ala	Ala	Ala	Asp	Ile	Ala	Gly	Thr	Leu	Pro	Val	Met
625				630						635					640
Lys	Val	Ser	Asp	His	Leu	Thr	Trp	Leu	Ala	Glu	Ala	Met	Ile	Asp	Ala
				645					650					655	
Val	Val	Gln	Gln	Ala	Trp	Val	Gln	Met	Val	Ala	Arg	Tyr	Gly	Lys	Pro
		660						665					670		
Asn	His	Leu	Asn	Glu	Arg	Glu	Gly	Arg	Gly	Phe	Ala	Val	Val	Gly	Tyr
		675					680					685			
Gly	Lys	Leu	Gly	Gly	Trp	Glu	Leu	Gly	Tyr	Ser	Ser	Asp	Leu	Asp	Leu
690						695					700				
Ile	Phe	Leu	His	Asp	Cys	Pro	Met	Asp	Ala	Met	Thr	Asp	Gly	Glu	Arg
705				710						715					720
Glu	Ile	Asp	Gly	Arg	Gln	Phe	Tyr	Leu	Arg	Leu	Ala	Gln	Arg	Ile	Met
			725						730					735	
His	Leu	Phe	Ser	Thr	Arg	Thr	Ser	Ser	Gly	Ile	Leu	Tyr	Glu	Val	Asp
		740						745					750		
Ala	Arg	Leu	Arg	Pro	Ser	Gly	Ala	Ala	Gly	Met	Leu	Val	Thr	Ser	Ala
	755					760						765			
Glu	Ala	Phe	Ala	Asp	Tyr	Gln	Lys	Asn	Glu	Ala	Trp	Thr	Trp	Glu	His
770					775						780				
Gln	Ala	Leu	Val	Arg	Ala	Arg	Val	Val	Tyr	Gly	Asp	Pro	Gln	Leu	Thr
785				790						795					800
Ala	His	Phe	Asp	Ala	Val	Arg	Arg	Glu	Ile	Met	Thr	Leu	Pro	Arg	Glu
			805					810						815	
Gly	Lys	Thr	Leu	Gln	Thr	Glu	Val	Arg	Glu	Met	Arg	Glu	Lys	Met	Arg
		820						825					830		
Ala	His	Leu	Gly	Asn	Lys	His	Arg	Asp	Arg	Phe	Asp	Ile	Lys	Ala	Asp
	835					840						845			
Glu	Gly	Gly	Ile	Thr	Asp	Ile	Glu	Phe	Ile	Thr	Gln	Tyr	Leu	Val	Leu
850					855						860				
Arg	Tyr	Ala	His	Glu	Lys	Pro	Lys	Leu	Thr	Arg	Trp	Ser	Asp	Asn	Val
865				870						875					880
Arg	Ile	Leu	Glu	Leu	Leu	Ala	Gln	Asn	Asp	Ile	Met	Glu	Glu	Gln	Glu
			885					890						895	
Ala	Met	Ala	Leu	Thr	Arg	Ala	Tyr	Thr	Thr	Leu	Arg	Asp	Glu	Leu	His
		900					905						910		
His	Leu	Ala	Leu	Gln	Glu	Leu	Pro	Gly	His	Val	Ser	Glu	Asp	Cys	Phe
	915						920					925			

Thr Ala Glu Arg Glu Leu Val Arg Ala Ser Trp Gln Lys Trp Leu Val
 930 935 940
 Glu Glu
 945

<210> 327
 <211> 433
 <212> PRT
 <213> E. Coli

<400> 327
 Met Ala Gln Glu Ile Glu Leu Lys Phe Ile Val Asn His Ser Ala Val
 1 5 10 15
 Glu Ala Leu Arg Asp His Leu Asn Thr Leu Gly Gly Glu His His Asp
 20 25 30
 Pro Val Gln Leu Leu Asn Ile Tyr Tyr Glu Thr Pro Asp Asn Trp Leu
 35 40 45
 Arg Gly His Asp Met Gly Leu Arg Ile Arg Gly Glu Asn Gly Arg Tyr
 50 55 60
 Glu Met Thr Met Lys Val Ala Gly Arg Val Thr Gly Gly Leu His Gln
 65 70 75 80
 Arg Pro Glu Tyr Asn Val Ala Leu Ser Glu Pro Thr Leu Asp Leu Ala
 85 90 95
 Gln Leu Pro Thr Glu Val Trp Pro Asn Gly Glu Leu Pro Ala Asp Leu
 100 105 110
 Ala Ser Arg Val Gln Pro Leu Phe Ser Thr Asp Phe Tyr Arg Glu Lys
 115 120 125
 Trp Leu Val Ala Val Asp Gly Ser Gln Ile Glu Ile Ala Leu Asp Gln
 130 135 140
 Gly Glu Val Lys Ala Gly Glu Phe Ala Glu Pro Ile Cys Glu Leu Glu
 145 150 155 160
 Leu Glu Leu Leu Ser Gly Asp Thr Arg Ala Val Leu Lys Leu Ala Asn
 165 170 175
 Gln Leu Val Ser Gln Thr Gly Leu Arg Gln Gly Ser Leu Ser Lys Ala
 180 185 190
 Ala Arg Gly Tyr His Leu Ala Gln Gly Asn Pro Ala Arg Glu Ile Lys
 195 200 205
 Pro Thr Thr Ile Leu His Val Ala Ala Lys Ala Asp Val Glu Gln Gly
 210 215 220
 Leu Glu Ala Ala Leu Glu Leu Ala Leu Ala Gln Trp Gln Tyr His Glu
 225 230 235 240
 Glu Leu Trp Val Arg Gly Asn Asp Ala Ala Lys Glu Gln Val Leu Ala
 245 250 255
 Ala Ile Ser Leu Val Arg His Thr Leu Met Leu Phe Gly Gly Ile Val
 260 265 270
 Pro Arg Lys Ala Ser Thr His Leu Arg Asp Leu Leu Thr Gln Cys Glu
 275 280 285
 Ala Thr Ile Ala Ser Ala Val Ser Ala Val Thr Ala Val Tyr Ser Thr
 290 295 300
 Glu Thr Ala Met Ala Lys Leu Ala Leu Thr Glu Trp Leu Val Ser Lys
 305 310 315 320
 Ala Trp Gln Pro Phe Leu Asp Ala Lys Ala Gln Gly Lys Ile Ser Asp
 325 330 335
 Ser Phe Lys Arg Phe Ala Asp Ile His Leu Ser Arg His Ala Ala Glu
 340 345 350

Leu Lys Ser Val Phe Cys Gln Pro Leu Gly Asp Arg Tyr Arg Asp Gln
 355 360 365
 Leu Pro Arg Leu Thr Arg Asp Ile Asp Ser Ile Leu Leu Leu Ala Gly
 370 375 380
 Tyr Tyr Asp Pro Val Val Ala Gln Ala Trp Leu Glu Asn Trp Gln Gly
 385 390 395 400
 Leu His His Ala Ile Ala Thr Gly Gln Arg Ile Glu Ile Glu His Phe
 405 410 415
 Arg Asn Glu Ala Asn Asn Gln Glu Pro Phe Trp Leu His Ser Gly Lys
 420 425 430
 Arg

<210> 328
 <211> 70
 <212> PRT
 <213> E. Coli

<400> 328
 Met Ser Gly Lys Met Thr Gly Ile Val Lys Trp Phe Asn Ala Asp Lys
 1 5 10 15
 Gly Phe Gly Phe Ile Thr Pro Asp Asp Gly Ser Lys Asp Val Phe Val
 20 25 30
 His Phe Ser Ala Ile Gln Asn Asp Gly Tyr Lys Ser Leu Asp Glu Gly
 35 40 45
 Gln Lys Val Ser Phe Thr Ile Glu Ser Gly Ala Lys Gly Pro Ala Ala
 50 55 60
 Gly Asn Val Thr Ser Leu
 65 70

<210> 329
 <211> 523
 <212> PRT
 <213> E. Coli

<400> 329
 Met Arg Asp Ile Val Asp Pro Val Phe Ser Ile Gly Ile Ser Ser Leu
 1 5 10 15
 Trp Asp Glu Leu Arg His Met Pro Ala Gly Gly Val Trp Trp Phe Asn
 20 25 30
 Val Asp Arg His Glu Asp Ala Ile Ser Leu Ala Asn Gln Thr Ile Ala
 35 40 45
 Ser Gln Ala Glu Thr Ala His Val Ala Val Ile Ser Met Asp Ser Asp
 50 55 60
 Pro Ala Lys Ile Phe Gln Leu Asp Asp Ser Gln Gly Pro Glu Lys Ile
 65 70 75 80
 Lys Leu Phe Ser Met Leu Asn His Glu Lys Gly Leu Tyr Tyr Leu Thr
 85 90 95
 Arg Asp Leu Gln Cys Ser Ile Asp Pro His Asn Tyr Leu Phe Ile Leu
 100 105 110
 Val Cys Ala Asn Asn Ala Trp Gln Asn Ile Pro Ala Glu Arg Leu Arg
 115 120 125
 Ser Trp Leu Asp Lys Met Asn Lys Trp Ser Arg Leu Asn His Cys Ser

130	135	140
Leu Leu Val Ile Asn Pro Gly Asn Asn Asn Asp Lys Gln Phe Ser Leu		
145	150	155
Leu Leu Glu Glu Tyr Arg Ser Leu Phe Gly Leu Ala Ser Leu Arg Phe		160
	165	170
Gln Gly Asp Gln His Leu Leu Asp Ile Ala Phe Trp Cys Asn Glu Lys		175
	180	185
Gly Val Ser Ala Arg Gln Gln Leu Ser Val Gln Gln Gln Asn Gly Ile		190
	195	200
Trp Thr Leu Val Gln Ser Glu Glu Ala Glu Ile Gln Pro Arg Ser Asp		205
	210	215
Glu Lys Arg Ile Leu Ser Asn Val Ala Val Leu Glu Gly Ala Pro Pro		220
225	230	235
Leu Ser Glu His Trp Gln Leu Phe Asn Asn Asn Glu Val Leu Phe Asn		240
	245	250
Glu Ala Arg Thr Ala Gln Ala Ala Thr Val Val Phe Ser Leu Gln Gln		255
	260	265
Asn Ala Gln Ile Glu Pro Leu Ala Arg Ser Ile His Thr Leu Arg Arg		270
	275	280
Gln Arg Gly Ser Ala Met Lys Ile Leu Val Arg Glu Asn Thr Ala Ser		285
290	295	300
Leu Arg Ala Thr Asp Glu Arg Leu Leu Leu Ala Cys Gly Ala Asn Met		305
	310	315
Val Ile Pro Trp Asn Ala Pro Leu Ser Arg Cys Leu Thr Met Ile Glu		320
	325	330
Ser Val Gln Gly Gln Lys Phe Ser Arg Tyr Val Pro Glu Asp Ile Thr		335
	340	345
Thr Leu Leu Ser Met Thr Gln Pro Leu Lys Leu Arg Gly Phe Gln Lys		350
	355	360
Trp Asp Val Phe Cys Asn Ala Val Asn Asn Met Met Asn Asn Pro Leu		365
	370	375
Leu Pro Ala His Gly Lys Gly Val Leu Val Ala Leu Arg Pro Val Pro		380
385	390	395
Gly Ile Arg Val Glu Gln Ala Leu Thr Leu Cys Arg Pro Asn Arg Thr		400
	405	410
Gly Asp Ile Met Thr Ile Gly Gly Asn Arg Leu Val Leu Phe Leu Ser		415
	420	425
Phe Cys Arg Ile Asn Asp Leu Asp Thr Ala Leu Asn His Ile Phe Pro		430
	435	440
Leu Pro Thr Gly Asp Ile Phe Ser Asn Arg Met Val Trp Phe Glu Asp		445
450	455	460
Asp Gln Ile Ser Ala Glu Leu Val Gln Met Arg Leu Leu Ala Pro Glu		465
	470	475
Gln Trp Gly Met Pro Leu Pro Leu Thr Gln Ser Ser Lys Pro Val Ile		480
	485	490
Asn Ala Glu His Asp Gly Arg His Trp Arg Arg Ile Pro Glu Pro Met		495
	500	505
Arg Leu Leu Asp Asp Ala Val Glu Arg Ser Ser		510
	515	520

<210> 330

<211> 62

<212> PRT

<213> E. Coli

<400> 330

Met	Thr	Ile	Ser	Asp	Ile	Ile	Glu	Ile	Ile	Val	Val	Cys	Ala	Leu	Ile
1				5					10					15	
Phe	Phe	Pro	Leu	Gly	Tyr	Leu	Ala	Arg	His	Ser	Leu	Arg	Arg	Ile	Arg
			20					25					30		
Asp	Thr	Leu	Arg	Leu	Phe	Phe	Ala	Lys	Pro	Arg	Tyr	Val	Lys	Pro	Ala
		35					40					45			
Gly	Thr	Leu	Arg	Arg	Thr	Glu	Lys	Ala	Arg	Ala	Thr	Lys	Lys		
	50					55					60				

<210> 331
 <211> 559
 <212> PRT
 <213> E. Coli

<400> 331

Met	Thr	Gln	Phe	Thr	Gln	Asn	Thr	Ala	Met	Pro	Ser	Ser	Leu	Trp	Gln
1				5					10					15	
Tyr	Trp	Arg	Gly	Leu	Ser	Gly	Trp	Asn	Phe	Tyr	Phe	Leu	Val	Lys	Phe
			20					25					30		
Gly	Leu	Leu	Trp	Ala	Gly	Tyr	Leu	Asn	Phe	His	Pro	Leu	Leu	Asn	Leu
		35					40					45			
Val	Phe	Ala	Ala	Phe	Leu	Leu	Met	Pro	Leu	Pro	Arg	Tyr	Ser	Leu	His
	50					55					60				
Arg	Leu	Arg	His	Trp	Ile	Ala	Leu	Pro	Ile	Gly	Phe	Ala	Leu	Phe	Trp
65					70					75					80
His	Asp	Thr	Trp	Leu	Pro	Gly	Pro	Glu	Ser	Ile	Met	Ser	Gln	Gly	Ser
				85					90					95	
Gln	Val	Ala	Gly	Phe	Ser	Thr	Asp	Tyr	Leu	Ile	Asp	Leu	Val	Thr	Arg
			100					105					110		
Phe	Ile	Asn	Trp	Gln	Met	Ile	Gly	Ala	Ile	Phe	Val	Leu	Leu	Val	Ala
		115					120					125			
Trp	Leu	Phe	Leu	Ser	Gln	Trp	Ile	Arg	Ile	Thr	Val	Phe	Val	Val	Ala
	130					135					140				
Ile	Leu	Leu	Trp	Leu	Asn	Val	Leu	Thr	Leu	Ala	Gly	Pro	Ser	Phe	Ser
145					150					155					160
Leu	Trp	Pro	Ala	Gly	Gln	Pro	Thr	Thr	Thr	Val	Thr	Thr	Thr	Gly	Gly
				165					170					175	
Asn	Ala	Ala	Ala	Thr	Val	Ala	Ala	Thr	Gly	Gly	Ala	Pro	Val	Val	Gly
		180						185					190		
Asp	Met	Pro	Ala	Gln	Thr	Ala	Pro	Pro	Thr	Thr	Ala	Asn	Leu	Asn	Ala
		195					200					205			
Trp	Leu	Asn	Asn	Phe	Tyr	Asn	Ala	Glu	Ala	Lys	Arg	Lys	Ser	Thr	Phe
	210					215					220				
Pro	Ser	Ser	Leu	Pro	Ala	Asp	Ala	Gln	Pro	Phe	Glu	Leu	Leu	Val	Ile
225					230					235					240
Asn	Ile	Cys	Ser	Leu	Ser	Trp	Ser	Asp	Ile	Glu	Ala	Ala	Gly	Leu	Met
			245					250					255		
Ser	His	Pro	Leu	Trp	Ser	His	Phe	Asp	Ile	Glu	Phe	Lys	Asn	Phe	Asn
			260					265					270		
Ser	Ala	Thr	Ser	Tyr	Ser	Gly	Pro	Ala	Ala	Ile	Arg	Leu	Leu	Arg	Ala
		275					280					285			
Ser	Cys	Gly	Gln	Thr	Ser	His	Thr	Asn	Leu	Tyr	Gln	Pro	Ala	Asn	Asn
	290					295					300				
Asp	Cys	Tyr	Leu	Phe	Asp	Asn	Leu	Ser	Lys	Leu	Gly	Phe	Thr	Gln	His
305					310					315					320
Leu	Met	Met	Gly	His	Asn	Gly	Gln	Phe	Gly	Gly	Phe	Leu	Lys	Glu	Val

				325					330				335				
Arg	Glu	Asn	Gly	Gly	Met	Gln	Ser	Glu	Leu	Met	Asp	Gln	Thr	Asn	Leu		
			340					345					350				
Pro	Val	Ile	Leu	Leu	Gly	Phe	Asp	Gly	Ser	Pro	Val	Tyr	Asp	Asp	Thr		
		355					360					365					
Ala	Val	Leu	Asn	Arg	Trp	Leu	Asp	Val	Thr	Glu	Lys	Asp	Lys	Asn	Ser		
	370					375					380						
Arg	Ser	Ala	Thr	Phe	Tyr	Asn	Thr	Leu	Pro	Leu	His	Asp	Gly	Asn	His		
385					390					395					400		
Tyr	Pro	Gly	Val	Ser	Lys	Thr	Ala	Asp	Tyr	Lys	Ala	Arg	Ala	Gln	Lys		
			405					410						415			
Phe	Phe	Asp	Glu	Leu	Asp	Ala	Phe	Phe	Thr	Glu	Leu	Glu	Lys	Ser	Gly		
		420						425					430				
Arg	Lys	Val	Met	Val	Val	Val	Val	Pro	Glu	His	Gly	Gly	Ala	Leu	Lys		
	435					440						445					
Gly	Asp	Arg	Met	Gln	Val	Ser	Gly	Leu	Arg	Asp	Ile	Pro	Ser	Pro	Ser		
	450				455					460							
Ile	Thr	Asp	Val	Pro	Val	Gly	Val	Lys	Phe	Phe	Gly	Met	Lys	Ala	Pro		
465				470					475						480		
His	Gln	Gly	Ala	Pro	Ile	Val	Ile	Glu	Gln	Pro	Ser	Ser	Phe	Leu	Ala		
			485					490						495			
Ile	Ser	Asp	Leu	Val	Val	Arg	Val	Leu	Asp	Gly	Lys	Ile	Phe	Thr	Glu		
	500						505					510					
Asp	Asn	Val	Asp	Trp	Lys	Lys	Leu	Thr	Ser	Gly	Leu	Pro	Gln	Thr	Ala		
	515						520					525					
Pro	Val	Ser	Glu	Asn	Ser	Asn	Ala	Val	Val	Ile	Gln	Tyr	Gln	Asp	Lys		
	530				535					540							
Pro	Tyr	Val	Arg	Leu	Asn	Gly	Gly	Asp	Trp	Val	Pro	Tyr	Pro	Gln			
545				550				555									

<210> 332
 <211> 127
 <212> PRT
 <213> E. Coli

Met	Glu	Gly	Ser	Arg	Met	Lys	Tyr	Arg	Ile	Ala	Leu	Ala	Val	Ser	Leu		
1				5					10					15			
Phe	Ala	Leu	Ser	Ala	Gly	Ser	Tyr	Ala	Thr	Thr	Leu	Cys	Gln	Glu	Lys		
		20					25						30				
Glu	Gln	Asn	Ile	Leu	Lys	Glu	Ile	Ser	Tyr	Ala	Glu	Lys	His	Gln	Asn		
		35				40						45					
Gln	Asn	Arg	Ile	Asp	Gly	Leu	Asn	Lys	Ala	Leu	Ser	Glu	Val	Arg	Ala		
	50				55					60							
Asn	Cys	Ser	Asp	Ser	Gln	Leu	Arg	Ala	Asp	His	Gln	Lys	Lys	Ile	Ala		
65				70					75						80		
Lys	Gln	Lys	Asp	Glu	Val	Ala	Glu	Arg	Gln	Gln	Asp	Leu	Ala	Glu	Ala		
			85				90							95			
Lys	Gln	Lys	Gly	Asp	Ala	Asp	Lys	Ile	Ala	Lys	Arg	Glu	Arg	Lys	Leu		
		100				105						110					
Ala	Glu	Ala	Gln	Glu	Glu	Leu	Lys	Lys	Leu	Glu	Ala	Arg	Asp	Tyr			
	115					120						125					

<210> 333
 <211> 101

<212> PRT
 <213> E. Coli

<400> 333
 Met Ser Lys Glu His Thr Thr Glu His Leu Arg Ala Glu Leu Lys Ser
 1 5 10 15
 Leu Ser Asp Thr Leu Glu Glu Val Leu Ser Ser Ser Gly Glu Lys Ser
 20 25 30
 Lys Glu Glu Leu Ser Lys Ile Arg Ser Lys Ala Glu Gln Ala Leu Lys
 35 40 45
 Gln Ser Arg Tyr Arg Leu Gly Glu Thr Gly Asp Ala Ile Ala Lys Gln
 50 55 60
 Thr Arg Val Ala Ala Ala Arg Ala Asp Glu Tyr Val Arg Glu Asn Pro
 65 70 75 80
 Trp Thr Gly Val Gly Ile Gly Ala Ala Ile Gly Val Val Leu Gly Val
 85 90 95
 Leu Leu Ser Arg Arg
 100

<210> 334
 <211> 134
 <212> PRT
 <213> E. Coli

<400> 334
 Met Ala Asp Thr His His Ala Gln Gly Pro Gly Lys Ser Val Leu Gly
 1 5 10 15
 Ile Gly Gln Arg Ile Val Ser Ile Met Val Glu Met Val Glu Thr Arg
 20 25 30
 Leu Arg Leu Ala Val Val Glu Leu Glu Glu Lys Ala Asn Leu Phe
 35 40 45
 Gln Leu Leu Leu Met Leu Gly Leu Thr Met Leu Phe Ala Ala Phe Gly
 50 55 60
 Leu Met Ser Leu Met Val Leu Ile Ile Trp Ala Val Asp Pro Gln Tyr
 65 70 75 80
 Arg Leu Asn Ala Met Ile Ala Thr Thr Val Val Leu Leu Leu Leu Ala
 85 90 95
 Leu Ile Gly Gly Ile Trp Thr Leu Arg Lys Ser Arg Lys Ser Thr Leu
 100 105 110
 Leu Arg His Thr Arg His Glu Leu Ala Asn Asp Arg Gln Leu Leu Glu
 115 120 125
 Glu Glu Ser Arg Glu Gln
 130

<210> 335
 <211> 99
 <212> PRT
 <213> E. Coli

<400> 335
 Met Ser Ser Lys Val Glu Arg Glu Arg Arg Lys Ala Gln Leu Leu Ser
 1 5 10 15
 Gln Ile Gln Gln Arg Leu Asp Leu Ser Ala Ser Arg Arg Glu Trp
 20 25 30

Leu Glu Thr Thr Gly Ala Tyr Asp Arg Arg Trp Asn Met Leu Leu Ser
 35 40 45
 Leu Arg Ser Trp Ala Leu Val Gly Ser Ser Val Met Ala Ile Trp Thr
 50 55 60
 Ile Arg His Pro Asn Met Leu Val Arg Trp Ala Arg Arg Gly Phe Gly
 65 70 75 80
 Val Trp Ser Ala Trp Arg Leu Val Lys Thr Thr Leu Lys Gln Gln Gln
 85 90 95
 Leu Arg Gly

<210> 336
 <211> 160
 <212> PRT
 <213> E. Coli

<400> 336
 Met Ile Leu Ser Ile Asp Ser Asn Asp Ala Asn Thr Ala Pro Leu His
 1 5 10 15
 Lys Lys Thr Ile Ser Ser Leu Ser Gly Ala Val Glu Ser Met Met Lys
 20 25 30
 Lys Leu Glu Asp Val Gly Val Leu Val Ala Arg Ile Leu Met Pro Ile
 35 40 45
 Leu Phe Ile Thr Ala Gly Trp Gly Lys Ile Thr Gly Tyr Ala Gly Thr
 50 55 60
 Gln Gln Tyr Met Glu Ala Met Gly Val Pro Gly Phe Met Leu Pro Leu
 65 70 75 80
 Val Ile Leu Leu Glu Phe Gly Gly Gly Leu Ala Ile Leu Phe Gly Phe
 85 90 95
 Leu Thr Arg Thr Thr Ala Leu Phe Thr Ala Gly Phe Thr Leu Leu Thr
 100 105 110
 Ala Phe Leu Phe His Ser Asn Phe Ala Glu Gly Val Asn Ser Leu Met
 115 120 125
 Phe Met Lys Asn Leu Thr Ile Ser Gly Gly Phe Leu Leu Leu Ala Ile
 130 135 140
 Thr Gly Pro Gly Ala Tyr Ser Ile Asp Arg Leu Leu Asn Lys Lys Trp
 145 150 155 160

<210> 337
 <211> 296
 <212> PRT
 <213> E. Coli

<400> 337
 Met Ile Lys Lys Thr Thr Glu Ile Asp Ala Ile Leu Leu Asn Leu Asn
 1 5 10 15
 Lys Ala Ile Asp Ala His Tyr Gln Trp Leu Val Ser Met Phe His Ser
 20 25 30
 Val Val Ala Arg Asp Ala Ser Lys Pro Glu Ile Thr Asp Asn His Ser
 35 40 45
 Tyr Gly Leu Cys Gln Phe Gly Arg Trp Ile Asp His Leu Gly Pro Leu
 50 55 60
 Asp Asn Asp Glu Leu Pro Tyr Val Arg Leu Met Asp Ser Ala His Gln

65					70					75					80
His	Met	His	Asn	Cys	Gly	Arg	Glu	Leu	Met	Leu	Ala	Ile	Val	Glu	Asn
				85					90					95	
His	Trp	Gln	Asp	Ala	His	Phe	Asp	Ala	Phe	Gln	Glu	Gly	Leu	Leu	Ser
			100					105					110		
Phe	Thr	Ala	Ala	Leu	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Leu	Thr	Ile	Arg
		115					120					125			
Ser	Asn	Met	Asp	Val	Leu	Thr	Gly	Leu	Pro	Gly	Arg	Arg	Val	Leu	Asp
	130					135					140				
Glu	Ser	Phe	Asp	His	Gln	Leu	Arg	Asn	Ala	Glu	Pro	Leu	Asn	Leu	Tyr
145					150					155					160
Leu	Met	Leu	Leu	Asp	Ile	Asp	Arg	Phe	Lys	Leu	Val	Asn	Asp	Thr	Tyr
			165						170					175	
Gly	His	Leu	Ile	Gly	Asp	Val	Val	Leu	Arg	Thr	Leu	Ala	Thr	Tyr	Leu
		180						185					190		
Ala	Ser	Trp	Thr	Arg	Asp	Tyr	Glu	Thr	Val	Tyr	Arg	Tyr	Gly	Gly	Glu
	195						200					205			
Glu	Phe	Ile	Ile	Ile	Val	Lys	Ala	Ala	Asn	Asp	Glu	Glu	Ala	Cys	Arg
210						215					220				
Ala	Gly	Val	Arg	Ile	Cys	Gln	Leu	Val	Asp	Asn	His	Ala	Ile	Thr	His
225					230					235					240
Ser	Glu	Gly	His	Ile	Asn	Ile	Thr	Val	Thr	Ala	Gly	Val	Ser	Arg	Ala
			245						250					255	
Phe	Pro	Glu	Glu	Pro	Leu	Asp	Val	Val	Ile	Gly	Arg	Ala	Asp	Arg	Ala
		260					265						270		
Met	Tyr	Glu	Gly	Lys	Gln	Thr	Gly	Arg	Asn	Arg	Cys	Met	Phe	Ile	Asp
	275						280					285			
Glu	Gln	Asn	Val	Ile	Asn	Arg	Val								
	290					295									

<210> 338

<211> 203

<212> PRT

<213> E. Coli

<400> 338

Met	Arg	Leu	Arg	Val	Val	Pro	Gly	Phe	Ile	Ser	Pro	Pro	Pro	Gly	Phe
1				5					10					15	
Gly	Gly	Leu	Gly	Tyr	Thr	Pro	Thr	Ala	Arg	Ala	Cys	Val	Asn	Ile	Ser
			20					25					30		
Ile	Pro	Leu	Gln	Leu	Arg	Val	Ile	Asp	Met	Leu	Asp	Val	Phe	Thr	Pro
	35						40					45			
Leu	Leu	Lys	Leu	Phe	Ala	Asn	Glu	Pro	Leu	Glu	Arg	Leu	Met	Tyr	Thr
	50					55					60				
Ile	Ile	Ile	Phe	Gly	Leu	Thr	Leu	Trp	Leu	Ile	Pro	Lys	Glu	Phe	Thr
65				70					75					80	
Val	Ala	Phe	Asn	Ala	Tyr	Thr	Glu	Ile	Pro	Trp	Leu	Phe	Gln	Ile	Ile
			85						90				95		
Val	Phe	Ala	Phe	Ser	Phe	Val	Val	Ala	Ile	Ser	Phe	Ser	Arg	Leu	Arg
	100						105					110			
Ala	His	Ile	Gln	Lys	His	Tyr	Ser	Leu	Leu	Pro	Glu	Gln	Arg	Val	Leu
	115						120					125			
Leu	Arg	Leu	Ser	Glu	Lys	Glu	Ile	Ala	Val	Phe	Lys	Asp	Phe	Leu	Lys
	130					135					140				
Thr	Gly	Asn	Leu	Ile	Ile	Thr	Ser	Pro	Cys	Arg	Asn	Pro	Val	Met	Lys

145 150 155 160
 Lys Leu Glu Arg Lys Gly Ile Ile Gln His Gln Ser Asp Ser Ala Asn
 165 170 175
 Cys Ser Tyr Tyr Leu Val Thr Glu Lys Tyr Ser His Phe Met Lys Leu
 180 185 190
 Phe Trp Asn Ser Arg Ser Arg Arg Phe Asn Arg
 195 200

<210> 339
 <211> 58
 <212> PRT
 <213> E. Coli

<400> 339
 Met Leu Leu Gln Pro Ser Ala Arg Thr Ser Phe Gly Phe Lys Cys Phe
 1 5 10 15
 Ala Phe Gly Ile Arg His Gly Ser Glu Arg Ser Ile Leu Val Gly Glu
 20 25 30
 His Ala Ala His Gln Gly Phe Val Val Ala Glu Val Asp Phe Leu His
 35 40 45
 Phe Ala Asn Leu Thr Ser Cys Cys Tyr Val
 50 55

<210> 340
 <211> 1426
 <212> PRT
 <213> E. Coli

<400> 340
 Met Ser Gly Lys Pro Ala Ala Arg Gln Gly Asp Met Thr Gln Tyr Gly
 1 5 10 15
 Gly Pro Ile Val Gln Gly Ser Ala Gly Val Arg Ile Gly Ala Pro Thr
 20 25 30
 Gly Val Ala Cys Ser Val Cys Pro Gly Gly Met Thr Ser Gly Asn Pro
 35 40 45
 Val Asn Pro Leu Leu Gly Ala Lys Val Leu Pro Gly Glu Thr Asp Leu
 50 55 60
 Ala Leu Pro Gly Pro Leu Pro Phe Ile Leu Ser Arg Thr Tyr Ser Ser
 65 70 75 80
 Tyr Arg Thr Lys Thr Pro Ala Pro Val Gly Val Phe Gly Pro Gly Trp
 85 90 95
 Lys Ala Pro Ser Asp Ile Arg Leu Gln Leu Arg Asp Asp Gly Leu Ile
 100 105 110
 Leu Asn Asp Asn Gly Gly Arg Ser Ile His Phe Glu Pro Leu Leu Pro
 115 120 125
 Gly Glu Ala Val Tyr Ser Arg Ser Glu Ser Met Trp Leu Val Arg Gly
 130 135 140
 Gly Lys Ala Ala Gln Pro Asp Gly His Thr Leu Ala Arg Leu Trp Gly
 145 150 155 160
 Ala Leu Pro Pro Asp Ile Arg Leu Ser Pro His Leu Tyr Leu Ala Thr
 165 170 175
 Asn Ser Ala Gln Gly Pro Trp Trp Ile Leu Gly Trp Ser Glu Arg Val
 180 185 190
 Pro Gly Ala Glu Asp Val Leu Pro Ala Pro Leu Pro Pro Tyr Arg Val

His Ser Val Phe Ser Tyr Asp Ala Leu Asp Arg Leu Val Gln Gln Gly
 660 665 670
 Gly Phe Asp Gly Arg Thr Gln Arg Tyr His Tyr Asp Leu Thr Gly Lys
 675 680 685
 Leu Thr Gln Ser Glu Asp Glu Gly Leu Val Ile Leu Trp Tyr Tyr Asp
 690 695 700
 Glu Ser Asp Arg Ile Thr His Arg Thr Val Asn Gly Glu Pro Ala Glu
 705 710 715 720
 Gln Trp Gln Tyr Asp Gly His Gly Trp Leu Thr Asp Ile Ser His Leu
 725 730 735
 Ser Glu Gly His Arg Val Ala Val His Tyr Gly Tyr Asp Asp Lys Gly
 740 745 750
 Arg Leu Thr Gly Glu Cys Gln Thr Val Glu Asn Pro Glu Thr Gly Glu
 755 760 765
 Leu Leu Trp Gln His Glu Thr Lys His Ala Tyr Asn Glu Gln Gly Leu
 770 775 780
 Ala Asn Arg Val Thr Pro Asp Ser Leu Pro Pro Val Glu Trp Leu Thr
 785 790 795 800
 Tyr Gly Ser Gly Tyr Leu Ala Gly Met Lys Leu Gly Gly Thr Pro Leu
 805 810 815
 Val Glu Tyr Thr Arg Asp Arg Leu His Arg Glu Thr Val Arg Ser Phe
 820 825 830
 Gly Ser Met Ala Gly Ser Asn Ala Ala Tyr Glu Leu Thr Ser Thr Tyr
 835 840 845
 Thr Pro Ala Gly Gln Leu Gln Ser Gln His Leu Asn Ser Leu Val Tyr
 850 855 860
 Asp Arg Asp Tyr Gly Trp Ser Asp Asn Gly Asp Leu Val Arg Ile Ser
 865 870 875 880
 Gly Pro Arg Gln Thr Arg Glu Tyr Gly Tyr Ser Ala Thr Gly Arg Leu
 885 890 895
 Glu Ser Val Arg Thr Leu Ala Pro Asp Leu Asp Ile Arg Ile Pro Tyr
 900 905 910
 Ala Thr Asp Pro Ala Gly Asn Arg Leu Pro Asp Pro Glu Leu His Pro
 915 920 925
 Asp Ser Thr Leu Thr Val Trp Pro Asp Asn Arg Ile Ala Glu Asp Ala
 930 935 940
 His Tyr Val Tyr Arg His Asp Glu Tyr Gly Arg Leu Thr Glu Lys Thr
 945 950 955 960
 Asp Arg Ile Pro Ala Gly Val Ile Arg Thr Asp Asp Glu Arg Thr His
 965 970 975
 His Tyr His Tyr Asp Ser Gln His Arg Leu Val Phe Tyr Thr Arg Ile
 980 985 990
 Gln His Gly Glu Pro Leu Val Glu Ser Arg Tyr Leu Tyr Asp Pro Leu
 995 1000 1005
 Gly Arg Arg Met Ala Lys Arg Val Trp Arg Arg Glu Arg Asp Leu Thr
 1010 1015 1020
 Gly Trp Met Ser Leu Ser Arg Lys Pro Glu Val Thr Trp Tyr Gly Trp
 1025 1030 1035 1040
 Asp Gly Asp Arg Leu Thr Thr Val Gln Thr Asp Thr Thr Arg Ile Gln
 1045 1050 1055
 Thr Val Tyr Glu Pro Gly Ser Phe Thr Pro Leu Ile Arg Val Glu Thr
 1060 1065 1070
 Glu Asn Gly Glu Arg Glu Lys Ala Gln Arg Arg Ser Leu Ala Glu Thr
 1075 1080 1085
 Leu Gln Gln Glu Gly Ser Glu Asn Gly His Gly Val Val Phe Pro Ala
 1090 1095 1100
 Glu Leu Val Arg Leu Leu Asp Arg Leu Glu Glu Glu Ile Arg Ala Asp

Arg Tyr Arg Tyr Gly Glu Arg Ile Ala Glu Glu Glu Lys Pro Tyr Leu
65 70 75 80
Ile Thr Glu Leu Pro Asp Ser Trp Val Val Glu Gly Ala Lys Leu Pro
85 90 95
Tyr Glu Val Ala Gly Gly Val Phe Ile Ile Glu Ile Asn Lys Lys Asn
100 105 110
Gly Cys Val Leu Asn Phe Leu His Ser Lys
115 120

<210> 342
<211> 236
<212> PRT
<213> E. Coli

<400> 342
Met Leu Ala Leu Met Asp Ala Asp Gly Asn Ile Ala Trp Ser Gly Glu
1 5 10 15
Tyr Asp Glu Trp Gly Asn Gln Leu Asn Glu Glu Asn Pro His His Leu
20 25 30
His Gln Pro Tyr Arg Leu Pro Gly Gln Gln Tyr Asp Lys Glu Ser Gly
35 40 45
Leu Tyr Tyr Asn Arg Asn Arg Tyr Tyr Asp Pro Leu Gln Gly Arg Tyr
50 55 60
Ile Thr Gln Asp Pro Ile Gly Leu Glu Gly Gly Trp Ser Leu Tyr Ala
65 70 75 80
Tyr Pro Leu Asn Pro Val Asn Gly Ile Asp Pro Leu Gly Leu Ser Pro
85 90 95
Ala Asp Val Ala Leu Ile Arg Arg Lys Asp Gln Leu Asn His Gln Arg
100 105 110
Ala Trp Asp Ile Leu Ser Asp Thr Tyr Glu Asp Met Lys Arg Leu Asn
115 120 125
Leu Gly Gly Thr Asp Gln Phe Phe His Cys Met Ala Phe Cys Arg Val
130 135 140
Ser Lys Leu Asn Asp Ala Gly Val Ser Arg Ser Ala Lys Gly Leu Gly
145 150 155 160
Tyr Glu Lys Glu Ile Arg Asp Tyr Gly Leu Asn Leu Phe Gly Met Tyr
165 170 175
Gly Arg Lys Val Lys Leu Ser His Ser Glu Met Ile Glu Asp Asn Lys
180 185 190
Lys Asp Leu Ala Val Asn Asp His Gly Leu Thr Cys Pro Ser Thr Thr
195 200 205
Asp Cys Ser Asp Arg Cys Ser Asp Tyr Ile Asn Pro Glu His Lys Lys
210 215 220
Thr Ile Lys Ala Leu Gln Asp Ala Gly Tyr Leu Lys
225 230 235

<210> 343
<211> 86
<212> PRT
<213> E. Coli

<400> 343
Met Leu Ala Ile Ser Ser Asn Leu Ser Lys Met Ile Ile Phe Ile Phe
1 5 10 15
Ala Ile Ile Ile Ile Val Val Leu Cys Val Ile Thr Tyr Leu Tyr Leu

<210> 346
 <211> 91
 <212> PRT
 <213> E. Coli

<400> 346
 Met Ala Ser Val Ser Ile Ser Cys Pro Ser Cys Ser Ala Thr Asp Gly
 1 5 10 15
 Val Val Arg Asn Gly Lys Ser Thr Ala Gly His Gln Arg Tyr Leu Cys
 20 25 30
 Ser His Cys Arg Lys Thr Trp Gln Leu Gln Phe Thr Tyr Thr Ala Ser
 35 40 45
 Gln Pro Gly Thr His Gln Lys Ile Ile Asp Met Ala Met Asn Gly Val
 50 55 60
 Gly Cys Arg Ala Thr Ala Arg Ile Met Gly Val Gly Leu Asn Thr Ile
 65 70 75 80
 Leu Arg His Leu Lys Asn Ser Gly Arg Ser Arg
 85 90

<210> 347
 <211> 138
 <212> PRT
 <213> E. Coli

<400> 347
 Met Met Thr Lys Thr Gln Ile Asn Lys Leu Ile Lys Met Met Asn Asp
 1 5 10 15
 Leu Asp Tyr Pro Phe Glu Ala Pro Leu Lys Glu Ser Phe Ile Glu Ser
 20 25 30
 Ile Ile Gln Ile Glu Phe Asn Ser Asn Ser Thr Asn Cys Leu Glu Lys
 35 40 45
 Leu Cys Asn Glu Val Ser Ile Leu Phe Lys Asn Gln Pro Asp Tyr Leu
 50 55 60
 Thr Phe Leu Arg Ala Met Asp Gly Phe Glu Val Asn Gly Leu Arg Leu
 65 70 75 80
 Phe Ser Leu Ser Ile Pro Glu Pro Ser Val Lys Asn Leu Phe Ala Val
 85 90 95
 Asn Glu Phe Tyr Arg Asn Asn Asp Asp Phe Ile Asn Pro Asp Leu Gln
 100 105 110
 Glu Arg Leu Val Ile Gly Asp Tyr Ser Ile Ser Ile Phe Thr Tyr Asp
 115 120 125
 Ile Lys Gly Asp Ala Ala Asn Leu Leu Ile
 130 135

<210> 348
 <211> 392
 <212> PRT
 <213> E. Coli

<400> 348
 Met Ser Asn Ile Val Tyr Leu Thr Val Thr Gly Glu Gln Gln Gly Ser
 1 5 10 15

Met	Val	Leu	Ala	Leu	Asn	Tyr	Asn	Met	His	Gly	Val	Asn	Ile	Arg	Ser
1				5					10					15	
Glu	Asn	Ala	Ala	Lys	Pro	His	Thr	Met	Pro	Ser	Arg	Tyr	Leu	Cys	Glu
		20						25					30		
Tyr	Ile	Arg	Ser	Ile	Glu	Lys	Asn	Gly	His	Ala	Leu	Asp	Phe	Gly	Cys
	35						40					45			
Gly	Lys	Leu	Arg	Tyr	Ser	Asp	Glu	Leu	Ile	Ser	Lys	Phe	Asp	Glu	Val
	50					55					60				
Thr	Phe	Leu	Asp	Ser	Lys	Arg	Gln	Leu	Glu	Arg	Glu	Gln	Ile	Ile	Arg
65					70					75					80
Gly	Ile	Lys	Thr	Lys	Ile	Ile	Asp	Tyr	Val	Pro	Arg	Tyr	Tyr	Lys	Asn
				85					90					95	
Ala	Asn	Thr	Val	Ala	Phe	Glu	Asp	Val	Asp	Lys	Ile	Ile	Gly	Gly	Tyr
			100					105					110		
Asp	Phe	Ile	Leu	Cys	Ser	Asn	Val	Leu	Ser	Ala	Val	Pro	Cys	Arg	Asp
	115						120					125			
Thr	Ile	Asp	Lys	Ile	Val	Leu	Ser	Ile	Lys	Arg	Leu	Leu	Lys	Ser	Gly
	130					135					140				
Gly	Glu	Thr	Leu	Ile	Val	Asn	Gln	Tyr	Lys	Ser	Ser	Tyr	Phe	Lys	Lys
145					150					155					160
Tyr	Glu	Thr	Gly	Arg	Lys	His	Leu	Tyr	Gly	Tyr	Ile	Tyr	Lys	Asn	Ser
			165						170					175	
Lys	Ser	Val	Ser	Tyr	Tyr	Gly	Leu	Leu	Asp	Glu	Leu	Ala	Val	Gln	Glu
			180					185					190		
Ile	Cys	Ser	Ser	His	Gly	Leu	Glu	Ile	Leu	Lys	Ser	Trp	Ser	Lys	Ala
	195						200					205			
Gly	Ser	Ser	Tyr	Val	Thr	Val	Gly	Ser	Cys	Asn	Ala	Ile			
	210					215					220				

<210> 350

<211> 234

<212> PRT

<213> E. Coli

<400> 350

Met	Asn	Asn	Met	Phe	Glu	Pro	Pro	Lys	Asn	Tyr	Asn	Glu	Met	Leu	Pro
1				5					10					15	
Lys	Leu	His	Lys	Ala	Thr	Phe	Leu	Asn	Thr	Leu	Ile	Tyr	Cys	Ile	Leu
			20					25					30		
Leu	Val	Ile	Tyr	Glu	Tyr	Ile	Pro	Leu	Ile	Thr	Leu	Pro	Thr	Lys	Tyr
		35					40					45			
Val	Pro	Pro	Ile	Lys	Asp	His	Glu	Ser	Phe	Ile	Asn	Trp	Ala	Leu	Ser
	50					55					60				
Phe	Gly	Ile	Leu	Pro	Cys	Ala	Phe	Ala	Ile	Phe	Ala	Tyr	Leu	Ile	Ser
65					70					75					80
Gly	Ala	Leu	Asp	Leu	His	Asn	Asn	Ala	Ala	Lys	Leu	Leu	Arg	Val	Arg
				85					90					95	
Tyr	Leu	Trp	Asp	Lys	His	Leu	Ile	Ile	Lys	Pro	Leu	Ser	Arg	Arg	Ala
			100					105					110		
Gly	Val	Asn	Arg	Lys	Leu	Asn	Lys	Asp	Glu	Ala	His	Asn	Val	Met	Ser
		115					120					125			
Asn	Leu	Tyr	Tyr	Pro	Glu	Val	Arg	Lys	Ile	Glu	Asp	Lys	His	Tyr	Ile
	130					135					140				
Glu	Leu	Phe	Trp	Asn	Lys	Val	Tyr	Tyr	Phe	Trp	Ile	Phe	Phe	Glu	Phe
145					150					155					160
Ser	Ile	Ile	Ala	Leu	Ile	Ser	Phe	Leu	Ile	Ile	Phe	Phe	Cys	Lys	Gln

				165					170				175			
Met	Asp	Ile	Phe	His	Val	Glu	Gly	Ser	Leu	Leu	Ser	Leu	Phe	Phe	Phe	
			180					185					190			
Val	Ile	Leu	Ser	Phe	Ser	Val	Ser	Gly	Ile	Ile	Phe	Ala	Leu	Thr	Val	
		195					200					205				
Lys	Pro	Arg	Thr	Glu	Ser	Gln	Val	Gly	Lys	Ile	Pro	Asp	Asp	Lys	Ile	
	210					215					220					
Lys	Glu	Phe	Phe	Thr	Lys	Asn	Asn	Ile	Asn							
225					230											

<210> 351
 <211> 94
 <212> PRT
 <213> E. Coli

Met	Phe	Thr	Ile	Asn	Ala	Glu	Val	Arg	Lys	Glu	Gln	Gly	Lys	Gly	Ala	
1				5					10					15		
Ser	Arg	Arg	Leu	Arg	Ala	Ala	Asn	Lys	Phe	Pro	Ala	Ile	Ile	Tyr	Gly	
			20					25					30			
Gly	Lys	Glu	Ala	Pro	Leu	Ala	Ile	Glu	Leu	Asp	His	Asp	Lys	Val	Met	
		35					40					45				
Asn	Met	Gln	Ala	Lys	Ala	Glu	Phe	Tyr	Ser	Glu	Val	Leu	Thr	Ile	Val	
	50					55					60					
Val	Asp	Gly	Lys	Glu	Ile	Lys	Val	Lys	Ala	Gln	Asp	Val	Gln	Arg	His	
65					70					75					80	
Pro	Tyr	Lys	Pro	Lys	Leu	Gln	His	Ile	Asp	Phe	Val	Arg	Ala			
				85					90							

<210> 352
 <211> 658
 <212> PRT
 <213> E. Coli

Met	Val	Leu	Phe	Tyr	Arg	Ala	His	Trp	Arg	Asp	Tyr	Lys	Asn	Asp	Gln	
1				5					10					15		
Val	Arg	Ile	Met	Met	Asn	Leu	Thr	Thr	Leu	Thr	His	Arg	Asp	Ala	Leu	
			20					25					30			
Cys	Leu	Asn	Ala	Arg	Phe	Thr	Ser	Arg	Glu	Glu	Ala	Ile	His	Ala	Leu	
		35					40					45				
Thr	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Lys	Ile	Ser	Ser	Thr	Glu	Gln	Phe	
	50					55					60					
Leu	Glu	Glu	Val	Tyr	Arg	Arg	Glu	Ser	Leu	Gly	Pro	Thr	Ala	Leu	Gly	
65					70					75					80	
Glu	Gly	Leu	Ala	Val	Pro	His	Gly	Lys	Thr	Ala	Ala	Val	Lys	Glu	Ala	
				85					90					95		
Ala	Phe	Ala	Val	Ala	Thr	Leu	Ser	Glu	Pro	Leu	Gln	Trp	Glu	Gly	Val	
			100					105					110			
Asp	Gly	Pro	Glu	Ala	Val	Asp	Leu	Val	Val	Leu	Leu	Ala	Ile	Pro	Pro	
		115					120					125				
Asn	Glu	Ala	Gly	Thr	Thr	His	Met	Gln	Leu	Leu	Thr	Ala	Leu	Thr	Thr	
	130					135					140					
Arg	Leu	Ala	Asp	Asp	Glu	Ile	Arg	Ala	Arg	Ile	Gln	Ser	Ala	Thr	Thr	

145	Pro	Asp	Glu	Leu	Leu	Ser	Ala	Leu	Asp	Asp	Lys	Gly	Gly	Thr	Gln	Pro
					165					170					175	
	Ser	Ala	Ser	Phe	Ser	Asn	Ala	Pro	Thr	Ile	Val	Cys	Val	Thr	Ala	Cys
				180					185					190		
	Pro	Ala	Gly	Ile	Ala	His	Thr	Tyr	Met	Ala	Ala	Glu	Tyr	Leu	Glu	Lys
			195					200					205			
	Ala	Gly	Arg	Lys	Leu	Gly	Val	Asn	Val	Tyr	Val	Glu	Lys	Gln	Gly	Ala
		210					215					220				
	Asn	Gly	Ile	Glu	Gly	Arg	Leu	Thr	Ala	Asp	Gln	Leu	Asn	Ser	Ala	Thr
225					230						235					240
	Ala	Cys	Ile	Phe	Ala	Ala	Glu	Val	Ala	Ile	Lys	Glu	Ser	Glu	Arg	Phe
				245					250						255	
	Asn	Gly	Ile	Pro	Ala	Leu	Ser	Val	Pro	Val	Ala	Glu	Pro	Ile	Arg	His
			260					265						270		
	Ala	Glu	Ala	Leu	Ile	Gln	Gln	Ala	Leu	Thr	Leu	Lys	Arg	Ser	Asp	Glu
		275					280					285				
	Thr	Arg	Thr	Val	Gln	Gln	Asp	Thr	Gln	Pro	Val	Lys	Ser	Val	Lys	Thr
		290					295					300				
	Glu	Leu	Lys	Gln	Ala	Leu	Leu	Ser	Gly	Ile	Ser	Phe	Ala	Val	Pro	Leu
305					310					315						320
	Ile	Val	Ala	Gly	Gly	Thr	Val	Leu	Ala	Val	Ala	Val	Leu	Leu	Ser	Gln
				325					330						335	
	Ile	Phe	Gly	Leu	Gln	Asp	Leu	Phe	Asn	Glu	Glu	Asn	Ser	Trp	Leu	Trp
			340					345						350		
	Met	Tyr	Arg	Lys	Leu	Gly	Gly	Gly	Leu	Leu	Gly	Ile	Leu	Met	Val	Pro
		355					360					365				
	Val	Leu	Ala	Ala	Tyr	Thr	Ala	Tyr	Ser	Leu	Ala	Asp	Lys	Pro	Ala	Leu
		370				375					380					
	Ala	Pro	Gly	Phe	Ala	Ala	Gly	Leu	Ala	Ala	Asn	Met	Ile	Gly	Ser	Gly
385					390					395						400
	Phe	Leu	Gly	Ala	Val	Val	Gly	Gly	Leu	Ile	Ala	Gly	Tyr	Leu	Met	Arg
				405					410						415	
	Trp	Val	Lys	Asn	His	Leu	Arg	Leu	Ser	Ser	Lys	Phe	Asn	Gly	Phe	Leu
			420					425					430			
	Thr	Phe	Tyr	Leu	Tyr	Pro	Val	Leu	Gly	Thr	Leu	Gly	Ala	Gly	Ser	Leu
		435					440					445				
	Met	Leu	Phe	Val	Val	Gly	Glu	Pro	Val	Ala	Trp	Ile	Asn	Asn	Ser	Leu
		450				455					460					
	Thr	Ala	Trp	Leu	Asn	Gly	Leu	Ser	Gly	Ser	Asn	Ala	Leu	Leu	Leu	Gly
465					470					475						480
	Ala	Ile	Leu	Gly	Phe	Met	Cys	Ser	Phe	Asp	Leu	Gly	Gly	Pro	Val	Asn
				485					490						495	
	Lys	Ala	Ala	Tyr	Ala	Phe	Cys	Leu	Gly	Ala	Met	Ala	Asn	Gly	Val	Tyr
			500					505					510			
	Gly	Pro	Tyr	Ala	Ile	Phe	Ala	Ser	Val	Lys	Met	Val	Ser	Ala	Phe	Thr
		515					520						525			
	Val	Thr	Ala	Ser	Thr	Met	Leu	Ala	Pro	Arg	Leu	Phe	Lys	Glu	Phe	Glu
		530				535					540					
	Ile	Glu	Thr	Gly	Lys	Ser	Thr	Trp	Leu	Leu	Gly	Leu	Ala	Gly	Ile	Thr
545					550					555						560
	Glu	Gly	Ala	Ile	Pro	Met	Ala	Ile	Glu	Asp	Pro	Leu	Arg	Val	Ile	Gly
				565					570						575	
	Ser	Phe	Val	Leu	Gly	Ser	Met	Val	Thr	Gly	Ala	Ile	Val	Gly	Ala	Met
			580					585					590			
	Asn	Ile	Gly	Leu	Ser	Thr	Pro	Gly	Ala	Gly	Ile	Phe	Ser	Leu	Phe	Leu
		595					600						605			

Leu His Asp Asn Gly Ala Gly Gly Val Met Ala Ala Ile Gly Trp Phe
 610 615 620
 Gly Ala Ala Leu Val Gly Ala Ala Ile Ser Thr Ala Ile Leu Leu Met
 625 630 635 640
 Trp Arg Arg His Ala Val Lys His Gly Asn Tyr Leu Thr Asp Gly Val
 645 650 655
 Met Pro

<210> 353
 <211> 877
 <212> PRT
 <213> E. Coli

<400> 353
 Met Lys Ala Val Ser Arg Val His Ile Thr Pro His Met His Trp Asp
 1 5 10 15
 Arg Glu Trp Tyr Phe Thr Thr Glu Glu Ser Arg Ile Leu Leu Val Asn
 20 25 30
 Asn Met Glu Glu Ile Leu Cys Arg Leu Glu Gln Asp Asn Glu Tyr Lys
 35 40 45
 Tyr Tyr Val Leu Asp Gly Gln Thr Ala Ile Leu Glu Asp Tyr Phe Ala
 50 55 60
 Val Lys Pro Glu Asn Lys Asp Arg Val Lys Lys Gln Val Glu Ala Gly
 65 70 75 80
 Lys Leu Ile Ile Gly Pro Trp Tyr Thr Gln Thr Asp Thr Thr Ile Val
 85 90 95
 Ser Ala Glu Ser Ile Val Arg Asn Leu Met Tyr Gly Met Arg Asp Cys
 100 105 110
 Leu Ala Phe Gly Glu Pro Met Lys Ile Gly Tyr Leu Pro Asp Ser Phe
 115 120 125
 Gly Met Ser Gly Gln Leu Pro His Ile Tyr Asn Gly Phe Gly Ile Thr
 130 135 140
 Arg Thr Met Phe Trp Arg Gly Cys Ser Glu Arg His Gly Thr Asp Lys
 145 150 155 160
 Thr Glu Phe Leu Trp Gln Ser Ser Asp Gly Ser Glu Val Thr Ala Gln
 165 170 175
 Val Leu Pro Leu Gly Tyr Ala Ile Gly Lys Tyr Leu Pro Ala Asp Glu
 180 185 190
 Asn Gly Leu Arg Lys Arg Leu Asp Ser Tyr Phe Asp Val Leu Glu Lys
 195 200 205
 Ala Ser Val Thr Lys Glu Ile Leu Leu Pro Asn Gly His Asp Gln Met
 210 215 220
 Pro Leu Gln Gln Asn Ile Phe Glu Val Met Asp Lys Leu Arg Glu Ile
 225 230 235 240
 Tyr Pro Gln Arg Lys Phe Val Met Ser Arg Phe Glu Glu Val Phe Glu
 245 250 255
 Lys Ile Glu Ala Gln Arg Asp Asn Leu Ala Thr Leu Lys Gly Glu Phe
 260 265 270
 Ile Asp Gly Lys Tyr Met Arg Val His Arg Thr Ile Gly Ser Thr Arg
 275 280 285
 Met Asp Ile Lys Ile Ala His Ala Arg Ile Glu Asn Lys Ile Val Asn
 290 295 300
 Leu Leu Glu Pro Leu Ala Thr Leu Ala Trp Thr Leu Gly Phe Glu Tyr
 305 310 315 320
 His His Gly Leu Leu Glu Lys Met Trp Lys Glu Ile Leu Lys Asn His

				325					330				335				
Ala	His	Asp	Ser	Ile	Gly	Cys	Cys	Cys	Ser	Asp	Lys	Val	His	Arg	Glu		
			340					345					350				
Ile	Val	Ala	Arg	Phe	Glu	Leu	Ala	Glu	Asp	Met	Ala	Asp	Asn	Leu	Ile		
		355					360					365					
Arg	Phe	Tyr	Met	Arg	Lys	Ile	Ala	Asp	Asn	Met	Pro	Gln	Ser	Asp	Ala		
	370					375					380						
Asp	Lys	Leu	Val	Leu	Phe	Asn	Leu	Met	Pro	Trp	Pro	Arg	Glu	Glu	Val		
385					390					395					400		
Ile	Asn	Thr	Thr	Val	Arg	Leu	Arg	Ala	Ser	Gln	Phe	Asn	Leu	Arg	Asp		
				405				410							415		
Asp	Arg	Gly	Gln	Pro	Val	Pro	Tyr	Phe	Ile	Arg	His	Ala	Arg	Glu	Ile		
		420						425				430					
Asp	Pro	Gly	Leu	Ile	Asp	Arg	Gln	Ile	Val	His	Tyr	Gly	Asn	Tyr	Asp		
		435					440					445					
Pro	Phe	Met	Glu	Phe	Asp	Ile	Gln	Ile	Asn	Gln	Ile	Val	Pro	Ser	Met		
	450					455					460						
Gly	Tyr	Arg	Thr	Leu	Tyr	Ile	Glu	Ala	Asn	Gln	Pro	Gly	Asn	Val	Ile		
465					470					475					480		
Ala	Ala	Lys	Ser	Asp	Ala	Glu	Gly	Ile	Leu	Glu	Asn	Ala	Phe	Trp	Gln		
				485				490						495			
Ile	Ala	Leu	Asn	Glu	Asp	Gly	Ser	Leu	Gln	Leu	Val	Asp	Lys	Asp	Ser		
			500					505					510				
Gly	Val	Arg	Tyr	Asp	Arg	Val	Leu	Gln	Ile	Glu	Glu	Ser	Ser	Asp	Asp		
		515					520					525					
Gly	Asp	Glu	Tyr	Asp	Tyr	Ser	Pro	Ala	Lys	Glu	Glu	Trp	Val	Ile	Thr		
	530					535					540						
Ala	Ala	Asn	Ala	Lys	Pro	Gln	Cys	Asp	Ile	Ile	His	Glu	Ala	Trp	Gln		
545					550					555					560		
Ser	Arg	Ala	Val	Ile	Arg	Tyr	Asp	Met	Ala	Val	Pro	Leu	Asn	Leu	Ser		
				565				570						575			
Glu	Arg	Ser	Ala	Arg	Gln	Ser	Thr	Gly	Arg	Val	Gly	Val	Val	Leu	Val		
			580					585					590				
Val	Thr	Leu	Ser	His	Asn	Ser	Arg	Arg	Ile	Asp	Val	Asp	Ile	Asn	Leu		
		595					600					605					
Asp	Asn	Gln	Ala	Asp	Asp	His	Arg	Leu	Arg	Val	Leu	Val	Pro	Thr	Pro		
	610					615					620						
Phe	Asn	Thr	Asp	Ser	Val	Leu	Ala	Asp	Thr	Gln	Phe	Gly	Ser	Leu	Thr		
625					630					635				640			
Arg	Pro	Val	Asn	Asp	Ser	Ala	Met	Asn	Asn	Trp	Gln	Gln	Glu	Gly	Trp		
				645					650					655			
Lys	Glu	Ala	Pro	Val	Pro	Val	Trp	Asn	Met	Leu	Asn	Tyr	Val	Ala	Leu		
			660					665					670				
Gln	Glu	Gly	Arg	Asn	Gly	Met	Ala	Val	Phe	Ser	Glu	Gly	Leu	Arg	Glu		
		675					680					685					
Phe	Glu	Val	Ile	Gly	Glu	Glu	Lys	Lys	Thr	Phe	Ala	Ile	Thr	Leu	Leu		
	690					695					700						
Arg	Gly	Val	Gly	Leu	Leu	Gly	Lys	Glu	Asp	Leu	Leu	Leu	Arg	Pro	Gly		
705					710					715				720			
Arg	Pro	Ser	Gly	Ile	Lys	Met	Pro	Val	Pro	Asp	Ser	Gln	Leu	Arg	Gly		
				725					730					735			
Leu	Leu	Ser	Cys	Arg	Leu	Ser	Leu	Leu	Ser	Tyr	Thr	Gly	Thr	Pro	Thr		
			740					745						750			
Ala	Ala	Gly	Val	Ala	Gln	Gln	Ala	Arg	Ala	Trp	Leu	Thr	Pro	Val	Gln		
		755					760					765					
Cys	Tyr	Asn	Lys	Ile	Pro	Trp	Asp	Val	Met	Lys	Leu	Asn	Lys	Ala	Gly		
	770					775					780						

Phe	Asn	Val	Pro	Glu	Ser	Tyr	Ser	Leu	Leu	Lys	Met	Pro	Pro	Val	Gly
785					790					795					800
Cys	Leu	Ile	Ser	Ala	Leu	Lys	Lys	Ala	Glu	Asp	Arg	Gln	Glu	Val	Ile
				805					810					815	
Leu	Arg	Leu	Phe	Asn	Pro	Ala	Glu	Ser	Ala	Thr	Cys	Asp	Ala	Thr	Val
			820				825						830		
Ala	Phe	Ser	Arg	Glu	Val	Ile	Ser	Cys	Ser	Glu	Thr	Met	Met	Asp	Glu
		835					840					845			
His	Ile	Thr	Thr	Glu	Glu	Asn	Gln	Gly	Ser	Asn	Leu	Ser	Gly	Pro	Phe
	850					855					860				
Leu	Pro	Gly	Gln	Ser	Arg	Thr	Phe	Ser	Tyr	Arg	Leu	Ala			
865					870					875					

<210> 354
 <211> 523
 <212> PRT
 <213> E. Coli

<400> 354

Met	Met	Leu	Asp	Ile	Val	Glu	Leu	Ser	Arg	Leu	Gln	Phe	Ala	Leu	Thr
1				5					10					15	
Ala	Met	Tyr	His	Phe	Leu	Phe	Val	Pro	Leu	Thr	Leu	Gly	Met	Ala	Phe
			20					25					30		
Leu	Leu	Ala	Ile	Met	Glu	Thr	Val	Tyr	Val	Leu	Ser	Gly	Lys	Gln	Ile
		35					40					45			
Tyr	Lys	Asp	Met	Thr	Lys	Phe	Trp	Gly	Lys	Leu	Phe	Gly	Ile	Asn	Phe
	50					55					60				
Ala	Leu	Gly	Val	Ala	Thr	Gly	Leu	Thr	Met	Glu	Phe	Gln	Phe	Gly	Thr
65					70					75					80
Asn	Trp	Ser	Tyr	Tyr	Ser	His	Tyr	Val	Gly	Asp	Ile	Phe	Gly	Ala	Pro
				85					90					95	
Leu	Ala	Ile	Glu	Gly	Leu	Met	Ala	Phe	Phe	Leu	Glu	Ser	Thr	Phe	Val
			100					105					110		
Gly	Leu	Phe	Phe	Phe	Gly	Trp	Asp	Arg	Leu	Gly	Lys	Val	Gln	His	Met
		115					120					125			
Cys	Val	Thr	Trp	Leu	Val	Ala	Leu	Gly	Ser	Asn	Leu	Ser	Ala	Leu	Trp
	130					135					140				
Ile	Leu	Val	Ala	Asn	Gly	Trp	Met	Gln	Asn	Pro	Ile	Ala	Ser	Asp	Phe
145					150					155					160
Asn	Phe	Glu	Thr	Met	Arg	Met	Glu	Met	Val	Ser	Phe	Ser	Glu	Leu	Val
				165					170					175	
Leu	Asn	Pro	Val	Ala	Gln	Val	Lys	Phe	Val	His	Thr	Val	Ala	Ser	Gly
			180					185					190		
Tyr	Val	Thr	Gly	Ala	Met	Phe	Ile	Leu	Gly	Ile	Ser	Ala	Trp	Tyr	Met
		195					200						205		
Leu	Lys	Gly	Arg	Asp	Phe	Ala	Phe	Ala	Lys	Arg	Ser	Phe	Ala	Ile	Ala
	210					215					220				
Ala	Ser	Phe	Gly	Met	Ala	Ala	Val	Leu	Ser	Val	Ile	Val	Leu	Gly	Asp
225					230					235					240
Glu	Ser	Gly	Tyr	Glu	Met	Gly	Asp	Val	Gln	Lys	Thr	Lys	Leu	Ala	Ala
				245					250					255	
Ile	Glu	Ala	Glu	Trp	Glu	Thr	Gln	Pro	Ala	Pro	Ala	Ala	Phe	Thr	Leu
			260					265					270		
Phe	Gly	Ile	Pro	Asp	Gln	Glu	Glu	Glu	Thr	Asn	Lys	Phe	Ala	Ile	Gln
	275						280					285			
Ile	Pro	Tyr	Ala	Leu	Gly	Ile	Ile	Ala	Thr	Arg	Ser	Val	Asp	Thr	Pro

290		295		300
Val Ile Gly Leu Lys	Glu Leu Met Val Gln His	Glu Glu Arg Ile Arg		
305	310	315	320	
Asn Gly Met Lys Ala	Tyr Ser Leu Leu Glu Gln Leu Arg Ser Gly Ser			
	325	330	335	
Thr Asp Gln Ala Val Arg Asp Gln Phe	Asn Ser Met Lys Lys Asp Leu			
	340	345	350	
Gly Tyr Gly Leu Leu Leu Lys Arg Tyr Thr Pro Asn Val Ala Asp Ala				
	355	360	365	
Thr Glu Ala Gln Ile Gln Gln Ala Thr Lys Asp Ser Ile Pro Arg Val				
	370	375	380	
Ala Pro Leu Tyr Phe Ala Phe Arg Ile Met Val Ala Cys Gly Phe Leu				
385	390	395	400	
Leu Leu Ala Ile Ile Ala Leu Ser Phe Trp Ser Val Ile Arg Asn Arg				
	405	410	415	
Ile Gly Glu Lys Lys Trp Leu Leu Arg Ala Ala Leu Tyr Gly Ile Pro				
	420	425	430	
Leu Pro Trp Ile Ala Val Glu Ala Gly Trp Phe Val Ala Glu Tyr Gly				
	435	440	445	
Arg Gln Pro Trp Ala Ile Gly Glu Val Leu Pro Thr Ala Val Ala Asn				
	450	455	460	
Ser Ser Leu Thr Ala Gly Asp Leu Ile Phe Ser Met Val Leu Ile Cys				
465	470	475	480	
Gly Leu Tyr Thr Leu Phe Leu Val Ala Glu Leu Phe Leu Met Phe Lys				
	485	490	495	
Phe Ala Arg Leu Gly Pro Ser Ser Leu Lys Thr Gly Arg Tyr His Phe				
	500	505	510	
Glu Gln Ser Ser Thr Thr Thr Gln Pro Ala Arg				
	515	520		

<210> 355

<211> 379

<212> PRT

<213> E. Coli

<400> 355

Met Ile Asp Tyr Glu Val Leu Arg Phe Ile Trp Trp Leu Leu Val Gly	
1	5
Val Leu Leu Ile Gly Phe Ala Val Thr Asp Gly Phe Asp Met Gly Val	
	20
Gly Met Leu Thr Arg Phe Leu Gly Arg Asn Asp Thr Glu Arg Arg Ile	
	35
Met Ile Asn Ser Ile Ala Pro His Trp Asp Gly Asn Gln Val Trp Leu	
50	55
Ile Thr Ala Gly Gly Ala Leu Phe Ala Ala Trp Pro Met Val Tyr Ala	
65	70
Ala Ala Phe Ser Gly Phe Tyr Val Ala Met Ile Leu Val Leu Ala Ser	
	85
Leu Phe Phe Arg Pro Val Gly Phe Asp Tyr Arg Ser Lys Ile Glu Glu	
	100
Thr Arg Trp Arg Asn Met Trp Asp Trp Gly Ile Phe Ile Gly Ser Phe	
	115
Val Pro Pro Leu Val Ile Gly Val Ala Phe Gly Asn Leu Leu Gln Gly	
130	135
Val Pro Phe Asn Val Asp Glu Tyr Leu Arg Leu Tyr Tyr Thr Gly Asn	
145	150
	155
	160

Phe	Phe	Gln	Leu	Leu	Asn	Pro	Phe	Gly	Leu	Leu	Ala	Gly	Val	Val	Ser
			165					170						175	
Val	Gly	Met	Ile	Ile	Thr	Gln	Gly	Ala	Thr	Tyr	Leu	Gln	Met	Arg	Thr
			180					185						190	
Val	Gly	Glu	Leu	His	Leu	Arg	Thr	Arg	Ala	Thr	Ala	Gln	Val	Ala	Ala
			195					200						205	
Leu	Val	Thr	Leu	Val	Cys	Phe	Ala	Leu	Ala	Gly	Val	Trp	Val	Met	Tyr
			210					215						220	
Gly	Ile	Asp	Gly	Tyr	Val	Val	Lys	Ser	Thr	Met	Asp	His	Tyr	Ala	Ala
225					230					235					240
Ser	Asn	Pro	Leu	Asn	Lys	Glu	Val	Val	Arg	Glu	Ala	Gly	Ala	Trp	Leu
				245					250						255
Val	Asn	Phe	Asn	Asn	Thr	Pro	Ile	Leu	Trp	Ala	Ile	Pro	Ala	Leu	Gly
			260					265						270	
Val	Val	Leu	Pro	Leu	Leu	Thr	Ile	Leu	Thr	Ala	Arg	Met	Asp	Lys	Ala
			275					280						285	
Ala	Trp	Ala	Phe	Val	Phe	Ser	Ser	Leu	Thr	Leu	Ala	Cys	Ile	Ile	Leu
			290					295				300			
Thr	Ala	Gly	Ile	Ala	Met	Phe	Pro	Phe	Val	Met	Pro	Ser	Ser	Thr	Met
305					310					315					320
Met	Asn	Ala	Ser	Leu	Thr	Met	Trp	Asp	Ala	Thr	Ser	Ser	Gln	Leu	Thr
				325					330						335
Leu	Asn	Val	Met	Thr	Trp	Val	Ala	Val	Val	Leu	Val	Pro	Ile	Ile	Leu
			340					345						350	
Leu	Tyr	Thr	Ala	Trp	Cys	Tyr	Trp	Lys	Met	Phe	Gly	Arg	Ile	Thr	Lys
			355				360					365			
Glu	Asp	Ile	Glu	Arg	Asn	Thr	His	Ser	Leu	Tyr					
			370				375								

<210> 356

<211> 456

<212> PRT

<213> E. Coli

<400> 356

Met	Glu	Leu	Ser	Ser	Leu	Thr	Ala	Val	Ser	Pro	Val	Asp	Gly	Arg	Tyr
1				5					10					15	
Gly	Asp	Lys	Val	Ser	Ala	Leu	Arg	Gly	Ile	Phe	Ser	Glu	Tyr	Gly	Leu
			20					25					30		
Leu	Lys	Phe	Arg	Val	Gln	Val	Glu	Val	Arg	Trp	Leu	Gln	Lys	Leu	Ala
			35				40					45			
Ala	His	Ala	Ala	Ile	Lys	Glu	Val	Pro	Ala	Phe	Ala	Ala	Asp	Ala	Ile
			50			55					60				
Gly	Tyr	Leu	Asp	Ala	Ile	Val	Ala	Ser	Phe	Ser	Glu	Glu	Asp	Ala	Ala
65					70					75					80
Arg	Ile	Lys	Thr	Ile	Glu	Arg	Thr	Thr	Asn	His	Asp	Val	Lys	Ala	Val
				85					90					95	
Glu	Tyr	Phe	Leu	Lys	Glu	Lys	Val	Ala	Glu	Ile	Pro	Glu	Leu	His	Ala
			100					105					110		
Val	Ser	Glu	Phe	Ile	His	Phe	Ala	Cys	Thr	Ser	Glu	Asp	Ile	Asn	Asn
			115				120					125			
Leu	Ser	His	Ala	Leu	Met	Leu	Lys	Thr	Ala	Arg	Asp	Glu	Val	Ile	Leu
			130			135					140				
Pro	Tyr	Trp	Arg	Gln	Leu	Ile	Asp	Gly	Ile	Lys	Asp	Leu	Ala	Val	Gln
145				150						155					160
Tyr	Arg	Asp	Ile	Pro	Leu	Leu	Ser	Arg	Thr	His	Gly	Gln	Pro	Ala	Thr

Pro	Ser	Thr	Ile	Gly	Lys	Glu	Met	Ala	Asn	Val	Ala	Tyr	Arg	Met	Glu
			180					185							
Arg	Gln	Tyr	Arg	Gln	Leu	Asn	Gln	Val	Glu	Ile	Leu	Gly	Lys	Ile	Asn
		195					200					205			
Gly	Ala	Val	Gly	Asn	Tyr	Asn	Ala	His	Ile	Ala	Ala	Tyr	Pro	Glu	Val
	210					215					220				
Asp	Trp	His	Gln	Phe	Ser	Glu	Glu	Phe	Val	Thr	Ser	Leu	Gly	Ile	Gln
225					230					235					240
Trp	Asn	Pro	Tyr	Thr	Thr	Gln	Ile	Glu	Pro	His	Asp	Tyr	Ile	Ala	Glu
				245					250						255
Leu	Phe	Asp	Cys	Val	Ala	Arg	Phe	Asn	Thr	Ile	Leu	Ile	Asp	Phe	Asp
		260						265					270		
Arg	Asp	Val	Trp	Gly	Tyr	Ile	Ala	Leu	Asn	His	Phe	Lys	Gln	Lys	Thr
		275					280					285			
Ile	Ala	Gly	Glu	Ile	Gly	Ser	Ser	Thr	Met	Pro	His	Lys	Val	Asn	Pro
	290					295					300				
Ile	Asp	Phe	Glu	Asn	Ser	Glu	Gly	Asn	Leu	Gly	Leu	Ser	Asn	Ala	Val
305					310					315					320
Leu	Gln	His	Leu	Ala	Ser	Lys	Leu	Pro	Val	Ser	Arg	Trp	Gln	Arg	Asp
				325					330					335	
Leu	Thr	Asp	Ser	Thr	Val	Leu	Arg	Asn	Leu	Gly	Val	Gly	Ile	Gly	Tyr
		340						345					350		
Ala	Leu	Ile	Ala	Tyr	Gln	Ser	Thr	Leu	Lys	Gly	Val	Ser	Lys	Leu	Glu
		355					360					365			
Val	Asn	Arg	Asp	His	Leu	Leu	Asp	Glu	Leu	Asp	His	Asn	Trp	Glu	Val
	370					375					380				
Leu	Ala	Glu	Pro	Ile	Gln	Thr	Val	Met	Arg	Arg	Tyr	Gly	Ile	Glu	Lys
385					390					395					400
Pro	Tyr	Glu	Lys	Leu	Lys	Glu	Leu	Thr	Arg	Gly	Lys	Arg	Val	Asp	Ala
				405					410					415	
Glu	Gly	Met	Lys	Gln	Phe	Ile	Asp	Gly	Leu	Ala	Leu	Pro	Glu	Glu	Glu
			420					425					430		
Lys	Ala	Arg	Leu	Lys	Ala	Met	Thr	Pro	Ala	Asn	Tyr	Ile	Gly	Arg	Ala
		435				440						445			
Ile	Thr	Met	Val	Asp	Glu	Leu	Lys								
	450					455									

<210> 357
 <211> 61
 <212> PRT
 <213> E. Coli

<400> 357
 Met Leu Ile Leu Thr Arg Arg Val Gly Glu Thr Leu Met Ile Gly Asp
 1 5 10 15
 Glu Val Thr Val Thr Val Leu Gly Val Lys Gly Asn Gln Val Arg Ile
 20 25 30
 Gly Val Asn Ala Pro Lys Glu Val Ser Val His Arg Glu Glu Ile Tyr
 35 40 45
 Gln Arg Ile Gln Ala Glu Lys Ser Gln Gln Ser Ser Tyr
 50 55 60

<210> 358
 <211> 93

<212> RNA
 <213> E. Coli

<400> 358
 ggugaggugg ccgagaggcu gaaggcgcuc ccugcuaag ggaguaugcg gucaaaagcu 60
 gcauccgggg uucgaauccc cgccucaccg cca 93

<210> 359
 <211> 200
 <212> PRT
 <213> E. Coli

<400> 359
 Met Lys Asn Lys Ala Asp Asn Lys Lys Arg Asn Phe Leu Thr His Ser
 1 5 10 15
 Glu Ile Glu Ser Leu Leu Lys Ala Ala Asn Thr Gly Pro His Ala Ala
 20 25 30
 Arg Asn Tyr Cys Leu Thr Leu Leu Cys Phe Ile His Gly Phe Arg Ala
 35 40 45
 Ser Glu Ile Cys Arg Leu Arg Ile Ser Asp Ile Asp Leu Lys Ala Lys
 50 55 60
 Cys Ile Tyr Ile His Arg Leu Lys Lys Gly Phe Ser Thr Thr His Pro
 65 70 75 80
 Leu Leu Asn Lys Glu Val Gln Ala Leu Lys Asn Trp Leu Ser Ile Arg
 85 90 95
 Thr Ser Tyr Pro His Ala`Glu Ser Glu Trp Val Phe Leu Ser Arg Lys
 100 105 110
 Gly Asn Pro Leu Ser Arg Gln Gln Phe Tyr His Ile Ile Ser Thr Ser
 115 120 125
 Gly Gly Asn Ala Gly Leu Ser Leu Glu Ile His Pro His Met Leu Arg
 130 135 140
 His Ser Cys Gly Phe Ala Leu Ala Asn Met Gly Ile Asp Thr Arg Leu
 145 150 155 160
 Ile Gln Asp Tyr Leu Gly His Arg Asn Ile Arg His Thr Val Trp Tyr
 165 170 175
 Thr Ala Ser Asn Ala Gly Arg Phe Tyr Gly Ile Trp Asp Arg Ala Arg
 180 185 190
 Gly Arg Gln Arg His Ala Val Leu
 195 200

<210> 360
 <211> 198
 <212> PRT
 <213> E. Coli

<400> 360
 Met Ser Lys Arg Arg Tyr Leu Thr Gly Lys Glu Val Gln Ala Met Met
 1 5 10 15
 Gln Ala Val Cys Tyr Gly Ala Thr Gly Ala Arg Asp Tyr Cys Leu Ile
 20 25 30
 Leu Leu Ala Tyr Arg His Gly Met Arg Ile Ser Glu Leu Leu Asp Leu
 35 40 45
 His Tyr Gln Asp Leu Asp Leu Asn Glu Gly Arg Ile Asn Ile Arg Arg
 50 55 60
 Leu Lys Asn Gly Phe Ser Thr Val His Pro Leu Arg Phe Asp Glu Arg

65					70					75				80	
Glu	Ala	Val	Glu	Arg	Trp	Thr	Gln	Glu	Arg	Ala	Asn	Trp	Lys	Gly	Ala
				85					90					95	
Asp	Arg	Thr	Asp	Ala	Ile	Phe	Ile	Ser	Arg	Arg	Gly	Ser	Arg	Leu	Ser
			100					105					110		
Arg	Gln	Gln	Ala	Tyr	Arg	Ile	Ile	Arg	Asp	Ala	Gly	Ile	Glu	Ala	Gly
		115					120					125			
Thr	Val	Thr	Gln	Thr	His	Pro	His	Met	Leu	Arg	His	Ala	Cys	Gly	Tyr
	130					135					140				
Glu	Leu	Ala	Glu	Arg	Gly	Ala	Asp	Thr	Arg	Leu	Ile	Gln	Asp	Tyr	Leu
145					150					155					160
Gly	His	Arg	Asn	Ile	Arg	His	Thr	Val	Arg	Tyr	Thr	Ala	Ser	Asn	Ala
			165						170					175	
Ala	Arg	Phe	Ala	Gly	Leu	Trp	Glu	Arg	Asn	Asn	Leu	Ile	Asn	Glu	Lys
			180					185					190		
Leu	Lys	Arg	Glu	Glu	Val										
			195												

<210> 361
 <211> 182
 <212> PRT
 <213> E. Coli

Met	Lys	Ile	Lys	Thr	Leu	Ala	Ile	Val	Val	Leu	Ser	Ala	Leu	Ser	Leu
1				5					10					15	
Ser	Ser	Thr	Ala	Ala	Leu	Ala	Ala	Ala	Thr	Thr	Val	Asn	Gly	Gly	Thr
			20					25					30		
Val	His	Phe	Lys	Gly	Glu	Val	Val	Asn	Ala	Ala	Cys	Ala	Val	Asp	Ala
		35					40					45			
Gly	Ser	Val	Asp	Gln	Thr	Val	Gln	Leu	Gly	Gln	Val	Arg	Thr	Ala	Ser
	50					55					60				
Leu	Ala	Gln	Glu	Gly	Ala	Thr	Ser	Ser	Ala	Val	Gly	Phe	Asn	Ile	Gln
65					70					75					80
Leu	Asn	Asp	Cys	Asp	Thr	Asn	Val	Ala	Ser	Lys	Ala	Ala	Val	Ala	Phe
			85						90					95	
Leu	Gly	Thr	Ala	Ile	Asp	Ala	Gly	His	Thr	Asn	Val	Leu	Ala	Leu	Gln
			100					105					110		
Ser	Ser	Ala	Ala	Gly	Ser	Ala	Thr	Asn	Val	Gly	Val	Gln	Ile	Leu	Asp
		115					120					125			
Arg	Thr	Gly	Ala	Ala	Leu	Thr	Leu	Asp	Gly	Ala	Thr	Phe	Ser	Ser	Glu
	130					135					140				
Thr	Thr	Leu	Asn	Asn	Gly	Thr	Asn	Thr	Ile	Pro	Phe	Gln	Ala	Arg	Tyr
145					150					155					160
Phe	Ala	Thr	Gly	Ala	Ala	Thr	Pro	Gly	Ala	Ala	Asn	Ala	Asp	Ala	Thr
			165						170					175	
Phe	Lys	Val	Gln	Tyr	Gln										
			180												

<210> 362
 <211> 215
 <212> PRT
 <213> E. Coli

<400> 362

Met	Leu	Leu	Met	Arg	Met	Arg	Pro	Ser	Arg	Phe	Ser	Ile	Asn	Asn	Leu
1			5					10					15		
Pro	Arg	Phe	Arg	Asp	Val	Ile	Thr	Gly	Arg	Asp	Ala	His	Pro	Cys	Ala
		20						25				30			
Ile	Lys	Ile	Thr	Met	Lys	Arg	Lys	Arg	Leu	Phe	Leu	Leu	Ala	Ser	Leu
	35					40					45				
Leu	Pro	Met	Phe	Ala	Leu	Ala	Gly	Asn	Lys	Trp	Asn	Thr	Thr	Leu	Pro
	50				55					60					
Gly	Gly	Asn	Met	Gln	Phe	Gln	Gly	Val	Ile	Ile	Ala	Glu	Thr	Cys	Arg
65				70					75					80	
Ile	Glu	Ala	Gly	Asp	Lys	Gln	Met	Thr	Val	Asn	Met	Gly	Gln	Ile	Ser
			85					90					95		
Ser	Asn	Arg	Phe	His	Ala	Val	Gly	Glu	Asp	Ser	Ala	Pro	Val	Pro	Phe
			100				105					110			
Val	Ile	His	Leu	Arg	Glu	Cys	Ser	Thr	Val	Val	Ser	Glu	Arg	Val	Gly
	115					120					125				
Val	Ala	Phe	His	Gly	Val	Ala	Asp	Gly	Lys	Asn	Pro	Asp	Val	Leu	Ser
	130				135					140					
Val	Gly	Glu	Gly	Pro	Gly	Ile	Ala	Thr	Asn	Ile	Gly	Val	Ala	Leu	Phe
145				150					155					160	
Asp	Asp	Glu	Gly	Asn	Leu	Val	Pro	Ile	Asn	Arg	Pro	Pro	Ala	Asn	Trp
			165				170						175		
Lys	Arg	Leu	Tyr	Ser	Gly	Ser	Thr	Ser	Leu	His	Phe	Ile	Ala	Lys	Tyr
		180					185					190			
Arg	Ala	Thr	Gly	Arg	Arg	Val	Thr	Gly	Gly	Ile	Ala	Asn	Ala	Gln	Ala
		195				200						205			
Trp	Phe	Ser	Leu	Thr	Tyr	Gln									
	210					215									

<210> 363

<211> 241

<212> PRT

<213> E. Coli

<400> 363

Met	Ser	Asn	Lys	Asn	Val	Asn	Val	Arg	Lys	Ser	Gln	Glu	Ile	Thr	Phe
1			5					10					15		
Cys	Leu	Leu	Ala	Gly	Ile	Leu	Met	Phe	Met	Ala	Met	Met	Val	Ala	Gly
		20						25				30			
Arg	Ala	Glu	Ala	Gly	Val	Ala	Leu	Gly	Ala	Thr	Arg	Val	Ile	Tyr	Pro
	35					40					45				
Ala	Gly	Gln	Lys	Gln	Glu	Gln	Leu	Ala	Val	Thr	Asn	Asn	Asp	Glu	Asn
	50			55						60					
Ser	Thr	Tyr	Leu	Ile	Gln	Ser	Trp	Val	Glu	Asn	Ala	Asp	Gly	Val	Lys
65				70					75					80	
Asp	Gly	Arg	Phe	Ile	Val	Thr	Pro	Pro	Leu	Phe	Ala	Met	Lys	Gly	Lys
			85					90					95		
Lys	Glu	Asn	Thr	Leu	Arg	Ile	Leu	Asp	Ala	Thr	Asn	Asn	Gln	Leu	Pro
		100					105					110			
Gln	Asp	Arg	Glu	Ser	Leu	Phe	Trp	Met	Asn	Val	Lys	Ala	Ile	Pro	Ser
	115					120					125				
Met	Asp	Lys	Ser	Lys	Leu	Thr	Glu	Asn	Thr	Leu	Gln	Leu	Ala	Ile	Ile
	130				135					140					
Ser	Arg	Ile	Lys	Leu	Tyr	Tyr	Arg	Pro	Ala	Lys	Leu	Ala	Leu	Pro	Pro

145		150		155		160
Asp	Gln	Ala	Ala	Glu	Lys	Leu
		165		170		175
Thr	Leu	Ile	Asn	Pro	Thr	Pro
		180		185		190
Ala	Gly	Thr	Arg	Val	Leu	Glu
		195		200		205
Ser	Thr	Val	Lys	Leu	Pro	Ser
		210		215		220
Thr	Ile	Asn	Asp	Tyr	Gly	Ala
225				230		235
Glu						240

<210> 364
 <211> 878
 <212> PRT
 <213> E. Coli

<400> 364

Met	Ser	Tyr	Leu	Asn	Leu	Arg	Leu	Tyr	Gln	Arg	Asn	Thr	Gln	Cys	Leu
1				5					10					15	
His	Ile	Arg	Lys	His	Arg	Leu	Ala	Gly	Phe	Phe	Val	Arg	Leu	Val	Val
			20					25					30		
Ala	Cys	Ala	Phe	Ala	Ala	Gln	Ala	Pro	Leu	Ser	Ser	Ala	Asp	Leu	Tyr
			35				40					45			
Phe	Asn	Pro	Arg	Phe	Leu	Ala	Asp	Asp	Pro	Gln	Ala	Val	Ala	Asp	Leu
			50			55					60				
Ser	Arg	Phe	Glu	Asn	Gly	Gln	Glu	Leu	Pro	Pro	Gly	Thr	Tyr	Arg	Val
65					70					75					80
Asp	Ile	Tyr	Leu	Asn	Asn	Gly	Tyr	Met	Ala	Thr	Arg	Asp	Val	Thr	Phe
				85					90					95	
Asn	Thr	Gly	Asp	Ser	Glu	Gln	Gly	Ile	Val	Pro	Cys	Leu	Thr	Arg	Ala
			100					105					110		
Gln	Leu	Ala	Ser	Met	Gly	Leu	Asn	Thr	Ala	Ser	Val	Ala	Gly	Met	Asn
			115				120					125			
Leu	Leu	Ala	Asp	Asp	Ala	Cys	Val	Pro	Leu	Thr	Thr	Met	Val	Gln	Asp
			130			135						140			
Ala	Thr	Ala	His	Leu	Asp	Val	Gly	Gln	Gln	Arg	Leu	Asn	Leu	Thr	Ile
145					150					155					160
Pro	Gln	Ala	Phe	Met	Ser	Asn	Arg	Ala	Arg	Gly	Tyr	Ile	Pro	Pro	Glu
				165					170						175
Leu	Trp	Asp	Pro	Gly	Ile	Asn	Ala	Gly	Leu	Leu	Asn	Tyr	Asn	Phe	Ser
			180					185					190		
Gly	Asn	Ser	Val	Gln	Asn	Arg	Ile	Gly	Gly	Asn	Ser	His	Tyr	Ala	Tyr
			195				200					205			
Leu	Asn	Leu	Gln	Ser	Gly	Leu	Asn	Ile	Gly	Ala	Trp	Arg	Leu	Arg	Asp
			210				215				220				
Asn	Thr	Thr	Trp	Ser	Tyr	Asn	Ser	Ser	Asp	Arg	Ser	Ser	Gly	Ser	Lys
225					230					235					240
Asn	Lys	Trp	Gln	His	Ile	Asn	Thr	Trp	Leu	Glu	Arg	Asp	Ile	Ile	Pro
				245					250					255	
Leu	Arg	Ser	Arg	Leu	Thr	Leu	Gly	Asp	Gly	Tyr	Thr	Gln	Gly	Asp	Ile
			260				265						270		
Phe	Asp	Gly	Ile	Asn	Phe	Arg	Gly	Ala	Gln	Leu	Ala	Ser	Asp	Asp	Asn
			275				280					285			

Met	Leu	Pro	Asp	Ser	Gln	Arg	Gly	Phe	Ala	Pro	Val	Ile	His	Gly	Ile	290	295	300
Ala	Arg	Gly	Thr	Ala	Gln	Val	Thr	Ile	Lys	Gln	Asn	Gly	Tyr	Asp	Ile	305	310	315
Tyr	Asn	Ser	Thr	Val	Pro	Pro	Gly	Pro	Phe	Thr	Ile	Asn	Asp	Ile	Tyr	325	330	335
Ala	Ala	Gly	Asn	Ser	Gly	Asp	Leu	Gln	Val	Thr	Ile	Lys	Glu	Ala	Asp	340	345	350
Gly	Ser	Thr	Gln	Ile	Phe	Thr	Val	Pro	Tyr	Ser	Ser	Val	Pro	Leu	Leu	355	360	365
Gln	Arg	Glu	Gly	His	Thr	Arg	Tyr	Ser	Ile	Thr	Ala	Gly	Glu	Tyr	Arg	370	375	380
Ser	Gly	Asn	Ala	Gln	Gln	Glu	Lys	Thr	Arg	Phe	Phe	Gln	Ser	Thr	Leu	385	390	395
Leu	His	Gly	Leu	Pro	Ala	Gly	Trp	Thr	Ile	Tyr	Gly	Gly	Thr	Gln	Leu	405	410	415
Ala	Asp	Arg	Tyr	Arg	Ala	Phe	Asn	Phe	Gly	Ile	Gly	Lys	Asn	Met	Gly	420	425	430
Ala	Leu	Gly	Ala	Leu	Ser	Val	Asp	Met	Thr	Gln	Ala	Asn	Ser	Thr	Leu	435	440	445
Pro	Asp	Asp	Ser	Gln	His	Asp	Gly	Gln	Ser	Val	Arg	Phe	Leu	Tyr	Asn	450	455	460
Lys	Ser	Leu	Asn	Glu	Ser	Gly	Thr	Asn	Ile	Gln	Leu	Val	Gly	Tyr	Arg	465	470	475
Tyr	Ser	Thr	Ser	Gly	Tyr	Phe	Asn	Phe	Ala	Asp	Thr	Thr	Tyr	Ser	Arg	485	490	495
Met	Asn	Gly	Tyr	Asn	Ile	Glu	Thr	Gln	Asp	Gly	Val	Ile	Gln	Val	Lys	500	505	510
Pro	Lys	Phe	Thr	Asp	Tyr	Tyr	Asn	Leu	Ala	Tyr	Asn	Lys	Arg	Gly	Lys	515	520	525
Leu	Gln	Leu	Thr	Val	Thr	Gln	Gln	Leu	Gly	Arg	Thr	Ser	Thr	Leu	Tyr	530	535	540
Leu	Ser	Gly	Ser	His	Gln	Thr	Tyr	Trp	Gly	Thr	Ser	Asn	Val	Asp	Glu	545	550	555
Gln	Phe	Gln	Ala	Gly	Leu	Asn	Thr	Ala	Phe	Glu	Asp	Ile	Asn	Trp	Thr	565	570	575
Leu	Ser	Tyr	Ser	Leu	Thr	Lys	Asn	Ala	Trp	Gln	Lys	Gly	Arg	Asp	Gln	580	585	590
Met	Leu	Ala	Leu	Asn	Val	Asn	Ile	Pro	Phe	Ser	His	Trp	Leu	Arg	Ser	595	600	605
Asp	Ser	Lys	Ser	Gln	Trp	Arg	His	Ala	Ser	Ala	Ser	Tyr	Ser	Met	Ser	610	615	620
His	Asp	Leu	Asn	Gly	Arg	Met	Thr	Asn	Leu	Ala	Gly	Val	Tyr	Gly	Thr	625	630	635
Leu	Leu	Glu	Asp	Asn	Asn	Leu	Ser	Tyr	Ser	Val	Gln	Thr	Gly	Tyr	Ala	645	650	655
Gly	Gly	Gly	Asp	Gly	Asn	Ser	Gly	Ser	Thr	Gly	Tyr	Ala	Thr	Leu	Asn	660	665	670
Tyr	Arg	Gly	Gly	Tyr	Gly	Asn	Ala	Asn	Ile	Gly	Tyr	Ser	His	Ser	Asp	675	680	685
Asp	Ile	Lys	Gln	Leu	Tyr	Tyr	Gly	Val	Ser	Gly	Gly	Val	Leu	Ala	His	690	695	700
Ala	Asn	Gly	Val	Thr	Leu	Gly	Gln	Pro	Leu	Asn	Asp	Thr	Val	Val	Leu	705	710	715
Val	Lys	Ala	Pro	Gly	Ala	Lys	Asp	Ala	Lys	Val	Glu	Asn	Gln	Thr	Gly	725	730	735
Val	Arg	Thr	Asp	Trp	Arg	Gly	Tyr	Ala	Val	Leu	Pro	Tyr	Ala	Thr	Glu			

			740					745				750			
Tyr	Arg	Glu	Asn	Arg	Val	Ala	Leu	Asp	Thr	Asn	Thr	Leu	Ala	Asp	Asn
		755					760					765			
Val	Asp	Leu	Asp	Asn	Ala	Val	Ala	Asn	Val	Val	Pro	Thr	Arg	Gly	Ala
	770					775					780				
Ile	Val	Arg	Ala	Glu	Phe	Lys	Ala	Arg	Val	Gly	Ile	Lys	Leu	Leu	Met
785					790					795					800
Thr	Leu	Thr	His	Asn	Asn	Lys	Pro	Leu	Pro	Phe	Gly	Ala	Met	Val	Thr
				805					810					815	
Ser	Glu	Ser	Ser	Gln	Ser	Ser	Gly	Ile	Val	Ala	Asp	Asn	Gly	Gln	Val
			820					825					830		
Tyr	Leu	Ser	Gly	Met	Pro	Leu	Ala	Gly	Lys	Val	Gln	Val	Lys	Trp	Gly
	835						840					845			
Glu	Glu	Glu	Asn	Ala	His	Cys	Val	Ala	Asn	Tyr	Gln	Leu	Pro	Pro	Glu
	850					855					860				
Ser	Gln	Gln	Gln	Leu	Leu	Thr	Gln	Leu	Ser	Ala	Glu	Cys	Arg		
865					870					875					

<210> 365
 <211> 176
 <212> PRT
 <213> E. Coli

Met	Arg	Asn	Lys	Pro	Phe	Tyr	Leu	Leu	Cys	Ala	Phe	Leu	Trp	Leu	Ala
1				5					10					15	
Val	Ser	His	Ala	Leu	Ala	Ala	Asp	Ser	Thr	Ile	Thr	Ile	Arg	Gly	Tyr
			20					25					30		
Val	Arg	Asp	Asn	Gly	Cys	Ser	Val	Ala	Ala	Glu	Ser	Thr	Asn	Phe	Thr
		35					40					45			
Val	Asp	Leu	Met	Glu	Asn	Ala	Ala	Lys	Gln	Phe	Asn	Asn	Ile	Gly	Ala
	50					55					60				
Thr	Thr	Pro	Val	Val	Pro	Phe	Arg	Ile	Leu	Leu	Ser	Pro	Cys	Gly	Asn
65					70					75					80
Ala	Val	Ser	Ala	Val	Lys	Val	Gly	Phe	Thr	Gly	Val	Ala	Asp	Ser	His
				85					90					95	
Asn	Ala	Asn	Leu	Leu	Ala	Leu	Glu	Asn	Thr	Val	Ser	Ala	Ala	Ser	Gly
			100					105					110		
Leu	Gly	Ile	Gln	Leu	Leu	Asn	Glu	Gln	Gln	Asn	Gln	Ile	Pro	Leu	Asn
	115						120					125			
Ala	Pro	Ser	Ser	Ala	Leu	Ser	Trp	Thr	Thr	Leu	Thr	Pro	Gly	Lys	Pro
	130					135					140				
Asn	Thr	Leu	Asn	Phe	Tyr	Ala	Arg	Leu	Met	Ala	Thr	Gln	Val	Pro	Val
145					150					155					160
Thr	Ala	Gly	His	Ile	Asn	Ala	Thr	Ala	Thr	Phe	Thr	Leu	Glu	Tyr	Gln
				165					170					175	

<210> 366
 <211> 167
 <212> PRT
 <213> E. Coli

<400> 366
 Met Lys Trp Cys Lys Arg Gly Tyr Val Leu Ala Ala Ile Leu Ala Leu

1				5					10					15	
Ala	Ser	Ala	Thr	Ile	Gln	Ala	Ala	Asp	Val	Thr	Ile	Thr	Val	Asn	Gly
			20					25					30		
Lys	Val	Val	Ala	Lys	Pro	Cys	Thr	Val	Ser	Thr	Thr	Asn	Ala	Thr	Val
		35					40					45			
Asp	Leu	Gly	Asp	Leu	Tyr	Ser	Phe	Ser	Leu	Met	Ser	Ala	Gly	Ala	Ala
	50					55					60				
Ser	Ala	Trp	His	Asp	Val	Ala	Leu	Glu	Leu	Thr	Asn	Cys	Pro	Val	Gly
65					70					75					80
Thr	Ser	Arg	Val	Thr	Ala	Ser	Phe	Ser	Gly	Ala	Ala	Asp	Ser	Thr	Gly
				85					90					95	
Tyr	Tyr	Lys	Asn	Gln	Gly	Thr	Ala	Gln	Asn	Ile	Gln	Leu	Glu	Leu	Gln
			100					105					110		
Asp	Asp	Ser	Gly	Asn	Thr	Leu	Asn	Thr	Gly	Ala	Thr	Lys	Thr	Val	Gln
		115					120					125			
Val	Asp	Asp	Ser	Ser	Gln	Ser	Ala	His	Phe	Pro	Leu	Gln	Val	Arg	Ala
	130					135					140				
Leu	Thr	Val	Asn	Gly	Gly	Ala	Thr	Gln	Gly	Thr	Ile	Gln	Ala	Val	Ile
145					150					155					160
Ser	Ile	Thr	Tyr	Thr	Tyr	Ser									
				165											

<210> 367

<211> 300

<212> PRT

<213> E. Coli

<400> 367

Met	Lys	Arg	Val	Ile	Thr	Leu	Phe	Ala	Val	Leu	Leu	Met	Gly	Trp	Ser
1				5					10					15	
Val	Asn	Ala	Trp	Ser	Phe	Ala	Cys	Lys	Thr	Ala	Asn	Gly	Thr	Ala	Ile
		20						25					30		
Pro	Ile	Gly	Gly	Gly	Ser	Ala	Asn	Val	Tyr	Val	Asn	Leu	Ala	Pro	Val
		35					40					45			
Val	Asn	Val	Gly	Gln	Asn	Leu	Val	Val	Asp	Leu	Ser	Thr	Gln	Ile	Phe
	50					55					60				
Cys	His	Asn	Asp	Tyr	Pro	Glu	Thr	Ile	Thr	Asp	Tyr	Val	Thr	Leu	Gln
65					70					75					80
Arg	Gly	Ser	Ala	Tyr	Gly	Gly	Val	Leu	Ser	Asn	Phe	Ser	Gly	Thr	Val
				85					90					95	
Lys	Tyr	Ser	Gly	Ser	Ser	Tyr	Pro	Phe	Pro	Thr	Thr	Ser	Glu	Thr	Pro
			100					105					110		
Arg	Val	Val	Tyr	Asn	Ser	Arg	Thr	Asp	Lys	Pro	Trp	Pro	Val	Ala	Leu
		115					120					125			
Tyr	Leu	Thr	Pro	Val	Ser	Ser	Ala	Gly	Gly	Val	Ala	Ile	Lys	Ala	Gly
	130					135					140				
Ser	Leu	Ile	Ala	Val	Leu	Ile	Leu	Arg	Gln	Thr	Asn	Asn	Tyr	Asn	Ser
145					150					155					160
Asp	Asp	Phe	Gln	Phe	Val	Trp	Asn	Ile	Tyr	Ala	Asn	Asn	Asp	Val	Val
				165					170					175	
Val	Pro	Thr	Gly	Gly	Cys	Asp	Val	Ser	Ala	Arg	Asp	Val	Thr	Val	Thr
			180					185					190		
Leu	Pro	Asp	Tyr	Pro	Gly	Ser	Val	Pro	Ile	Pro	Leu	Thr	Val	Tyr	Cys
		195					200					205			
Ala	Lys	Ser	Gln	Asn	Leu	Gly	Tyr	Tyr	Leu	Ser	Gly	Thr	Thr	Ala	Asp

210		215		220
Ala Gly Asn Ser Ile Phe Thr Asn Thr Ala Ser Phe Ser Pro Ala Gln				
225		230		235
Gly Val Gly Val Gln Leu Thr Arg Asn Gly Thr Ile Ile Pro Ala Asn				
	245		250	255
Asn Thr Val Ser Leu Gly Ala Val Gly Thr Ser Ala Val Ser Leu Gly				
	260		265	270
Leu Thr Ala Asn Tyr Ala Arg Thr Gly Gly Gln Val Thr Ala Gly Asn				
	275		280	285
Val Gln Ser Ile Ile Gly Val Thr Phe Val Tyr Gln				
290		295		300

<210> 368
 <211> 521
 <212> PRT
 <213> E. Coli

<400> 368

Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys	
1 5 10 15	
Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu	
20 25 30	
Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp	
35 40 45	
Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile	
50 55 60	
Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn	
65 70 75 80	
Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu	
85 90 95	
Ser Asn Asp Ser Arg Leu Thr Gly Cys Glu Arg Ser Pro Phe Glu Ser	
100 105 110	
Tyr Gly Asn Cys Ser Leu Thr Gly Gln Arg Thr Leu Arg Asn Phe Pro	
115 120 125	
Gly Cys Arg His Gly Pro Cys Arg Ser Cys Ala Gly Val Leu Gly Ser	
130 135 140	
Ser Gln Lys Glu Arg Pro Ala Ser Leu Pro Gly Ser Ser Arg Lys Ile	
145 150 155 160	
Val Arg Lys Ser Val Leu Ser Ala Ala Ser Val Leu Leu Asp Lys Ser	
165 170 175	
Cys Gln Ala Arg Ala Ser Ser Ser Ile Ser Met Asn Thr Lys Ile Arg	
180 185 190	
Tyr Gly Leu Ser Ala Ala Val Leu Ala Leu Ile Gly Ala Gly Ala Ser	
195 200 205	
Ala Pro Gln Ile Leu Asp Gln Phe Leu Asp Glu Lys Glu Gly Asn His	
210 215 220	
Thr Met Ala Tyr Arg Asp Gly Ser Gly Ile Trp Thr Ile Cys Arg Gly	
225 230 235 240	
Ala Thr Val Val Asp Gly Lys Thr Val Phe Pro Asn Met Lys Leu Ser	
245 250 255	
Lys Glu Lys Cys Asp Gln Val Asn Ala Ile Glu Arg Asp Lys Ala Leu	
260 265 270	
Ala Trp Val Glu Arg Asn Ile Lys Val Pro Leu Thr Glu Pro Gln Lys	
275 280 285	
Ala Gly Ile Ala Ser Phe Cys Pro Tyr Asn Ile Gly Pro Gly Lys Cys	

290		295		300											
Phe	Pro	Ser	Thr	Phe	Tyr	Lys	Arg	Leu	Asn	Ala	Gly	Asp	Arg	Lys	Gly
305					310					315					320
Ala	Cys	Glu	Ala	Ile	Arg	Trp	Trp	Ile	Lys	Asp	Gly	Gly	Arg	Asp	Cys
				325					330					335	
Arg	Ile	Arg	Ser	Asn	Asn	Cys	Tyr	Gly	Gln	Val	Ile	Arg	Arg	Asp	Gln
			340					345					350		
Glu	Ser	Ala	Leu	Thr	Cys	Trp	Gly	Ile	Glu	Gln	Ile	Arg	Tyr	Ser	Trp
		355					360					365			
Phe	Phe	Ser	Cys	Cys	Gln	Asp	Leu	Ser	Ser	Glu	Met	Ser	Gly	Ala	Thr
370						375					380				
Glu	Asp	Gly	Lys	Lys	Asn	Gly	Arg	Asn	Val	Met	Leu	Pro	His	Tyr	His
385					390					395					400
Lys	Arg	Met	Leu	Asn	Leu	Leu	Leu	Glu	Leu	Asn	Arg	Gly	Glu	Leu	Pro
				405					410					415	
Val	Met	Arg	Leu	Leu	Lys	Met	Arg	Asn	Arg	Asn	Leu	Leu	Lys	Phe	Leu
			420					425					430		
Pro	Gly	Leu	Leu	Ile	Cys	Leu	Ile	Val	Leu	Thr	Ser	Cys	Val	Pro	Lys
		435					440					445			
Gln	Lys	Asn	Met	Pro	Tyr	Ala	Leu	Thr	Gln	Arg	Ser	Ile	Pro	Gln	Ile
450						455					460				
Leu	Pro	Leu	Pro	Ser	Glu	Ala	Lys	Gln	Pro	Lys	Pro	Pro	Lys	Glu	Cys
465					470					475					480
Ser	Pro	Thr	Cys	Ser	Glu	Ile	Leu	Gln	Gln	Lys	Leu	Ser	Phe	Met	Leu
				485					490					495	
Lys	Leu	Leu	Thr	Asn	Ala	Thr	Ser	Gln	Glu	Leu	Val	Asn	Arg	Ser	Met
			500					505					510		
Asn	Leu	Glu	Ile	Lys	Ser	Ile	Lys	Cys							
		515					520								

<210> 369
 <211> 177
 <212> PRT
 <213> E. Coli

<400> 369

Met	Asn	Thr	Lys	Ile	Arg	Tyr	Gly	Leu	Ser	Ala	Ala	Val	Leu	Ala	Leu
1				5					10					15	
Ile	Gly	Ala	Gly	Ala	Ser	Ala	Pro	Gln	Ile	Leu	Asp	Gln	Phe	Leu	Asp
			20					25					30		
Glu	Lys	Glu	Gly	Asn	His	Thr	Met	Ala	Tyr	Arg	Asp	Gly	Ser	Gly	Ile
		35					40					45			
Trp	Thr	Ile	Cys	Arg	Gly	Ala	Thr	Val	Val	Asp	Gly	Lys	Thr	Val	Phe
	50					55					60				
Pro	Asn	Met	Lys	Leu	Ser	Lys	Glu	Lys	Cys	Asp	Gln	Val	Asn	Ala	Ile
65					70					75					80
Glu	Arg	Asp	Lys	Ala	Leu	Ala	Trp	Val	Glu	Arg	Asn	Ile	Lys	Val	Pro
				85					90					95	
Leu	Thr	Glu	Pro	Gln	Lys	Ala	Gly	Ile	Ala	Ser	Phe	Cys	Pro	Tyr	Asn
			100				105						110		
Ile	Gly	Pro	Gly	Lys	Cys	Phe	Pro	Ser	Thr	Phe	Tyr	Lys	Arg	Leu	Asn
	115						120					125			
Ala	Gly	Asp	Arg	Lys	Gly	Ala	Cys	Glu	Ala	Ile	Arg	Trp	Trp	Ile	Lys
130						135					140				
Asp	Gly	Gly	Arg	Asp	Cys	Arg	Ile	Arg	Ser	Asn	Asn	Cys	Tyr	Gly	Gln

145 150 155 160
 Val Ile Arg Arg Asp Gln Glu Ser Ala Leu Thr Cys Trp Gly Ile Glu
 165 170 175
 Gln

<210> 370
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 370
 Met Thr Gln Asp Tyr Glu Leu Val Val Lys Gly Val Arg Asn Phe Glu
 1 5 10 15
 Asn Lys Val Thr Val Thr Val Ala Leu Gln Asp Lys Glu Arg Phe Asp
 20 25 30
 Gly Glu Ile Phe Asp Leu Asp Val Ala Met Asp Arg Val Glu Gly Ala
 35 40 45
 Ala Leu Glu Phe Tyr Glu Ala Ala Arg Arg Ser Val Arg Gln Val
 50 55 60
 Phe Leu Glu Val Ala Glu Lys Leu Ser Glu Lys Val Glu Ser Tyr Leu
 65 70 75 80
 Gln His Gln Tyr Ser Phe Lys Ile Glu Asn Pro Ala Asn Lys His Glu
 85 90 95
 Arg Pro His His Lys Tyr Leu
 100

<210> 371
 <211> 96
 <212> PRT
 <213> E. Coli

<400> 371
 Met Leu Ser Lys Leu Pro Arg Arg Leu Arg Ser Phe Gln Thr Tyr Cys
 1 5 10 15
 Thr Ile Arg Val His Arg Gly Glu Asp Met Lys Ser Met Asp Lys Leu
 20 25 30
 Thr Thr Gly Val Ala Tyr Gly Thr Ser Ala Gly Asn Ala Gly Phe Trp
 35 40 45
 Ala Leu Gln Leu Leu Asp Lys Val Thr Pro Ser Gln Trp Ala Ala Ile
 50 55 60
 Gly Val Leu Gly Ser Leu Val Phe Gly Leu Leu Thr Tyr Leu Thr Asn
 65 70 75 80
 Leu Tyr Phe Lys Ile Lys Glu Asp Arg Arg Lys Ala Ala Arg Gly Glu
 85 90 95

<210> 372
 <211> 71
 <212> PRT
 <213> E. Coli

<400> 372

Met	Ser	Asn	Lys	Met	Thr	Gly	Leu	Val	Lys	Trp	Phe	Asn	Ala	Asp	Lys
1				5					10					15	
Gly	Phe	Gly	Phe	Ile	Ser	Pro	Val	Asp	Gly	Ser	Lys	Asp	Val	Phe	Val
			20					25					30		
His	Phe	Ser	Ala	Ile	Gln	Asn	Asp	Asn	Tyr	Arg	Thr	Leu	Phe	Glu	Gly
		35					40					45			
Gln	Lys	Val	Thr	Phe	Ser	Ile	Glu	Ser	Gly	Ala	Lys	Gly	Pro	Ala	Ala
	50					55					60				
Ala	Asn	Val	Ile	Ile	Thr	Asp									
65					70										

<210> 373
 <211> 338
 <212> PRT
 <213> E. Coli

<400> 373

Met	Phe	Val	Ile	Trp	Ser	His	Arg	Thr	Gly	Phe	Ile	Met	Ser	His	Gln
1				5					10					15	
Leu	Thr	Phe	Ala	Asp	Ser	Glu	Phe	Ser	Ser	Lys	Arg	Arg	Gln	Thr	Arg
			20					25					30		
Lys	Glu	Ile	Phe	Leu	Ser	Arg	Met	Glu	Gln	Ile	Leu	Pro	Trp	Gln	Asn
		35					40					45			
Met	Val	Glu	Val	Ile	Glu	Pro	Phe	Tyr	Pro	Lys	Ala	Gly	Asn	Gly	Arg
	50					55					60				
Arg	Pro	Tyr	Pro	Leu	Glu	Thr	Met	Leu	Arg	Ile	His	Cys	Met	Gln	His
65					70					75					80
Trp	Tyr	Asn	Leu	Ser	Asp	Gly	Ala	Met	Glu	Asp	Ala	Leu	Tyr	Glu	Ile
			85						90					95	
Ala	Ser	Met	Arg	Leu	Phe	Ala	Arg	Leu	Ser	Leu	Asp	Ser	Ala	Leu	Pro
			100					105					110		
Asp	Arg	Thr	Thr	Ile	Met	Asn	Phe	Arg	His	Leu	Leu	Glu	Gln	His	Gln
		115					120					125			
Leu	Ala	Arg	Gln	Leu	Phe	Lys	Thr	Ile	Asn	Arg	Trp	Leu	Ala	Glu	Ala
	130					135					140				
Gly	Val	Met	Met	Thr	Gln	Gly	Thr	Leu	Val	Asp	Ala	Thr	Ile	Ile	Glu
145					150					155					160
Ala	Pro	Ser	Ser	Thr	Lys	Asn	Lys	Glu	Gln	Gln	Arg	Asp	Pro	Glu	Met
				165					170					175	
His	Gln	Thr	Lys	Lys	Gly	Asn	Gln	Trp	His	Phe	Gly	Met	Lys	Ala	His
			180					185					190		
Ile	Gly	Val	Asp	Ala	Lys	Ser	Gly	Leu	Thr	His	Ser	Leu	Val	Thr	Thr
		195					200						205		
Ala	Ala	Asn	Glu	His	Asp	Leu	Asn	Gln	Leu	Gly	Asn	Leu	Leu	His	Gly
	210					215					220				
Glu	Glu	Gln	Phe	Val	Ser	Ala	Asp	Ala	Gly	Tyr	Gln	Gly	Ala	Pro	Gln
225					230					235					240
Arg	Glu	Glu	Leu	Ala	Glu	Val	Asp	Val	Asp	Trp	Leu	Ile	Ala	Glu	Arg
				245					250					255	
Pro	Gly	Lys	Val	Arg	Thr	Leu	Lys	Gln	His	Pro	Arg	Lys	Asn	Lys	Thr
			260					265					270		
Ala	Ile	Asn	Ile	Glu	Tyr	Met	Lys	Ala	Ser	Ile	Arg	Ala	Arg	Val	Glu
		275					280					285			
His	Pro	Phe	Arg	Ile	Ile	Lys	Arg	Gln	Phe	Gly	Phe	Val	Lys	Ala	Arg
	290					295					300				

Tyr Lys Gly Leu Leu Lys Asn Asp Asn Gln Leu Ala Met Leu Phe Thr
 305 310 315 320
 Leu Ala Asn Leu Phe Arg Ala Asp Gln Met Ile Arg Gln Trp Glu Arg
 325 330 335
 Ser His

<210> 374
 <211> 157
 <212> PRT
 <213> E. Coli

<400> 374
 Met Val Tyr Ile Ile Ile Val Ser His Gly His Glu Asp Tyr Ile Lys
 1 5 10 15
 Lys Leu Leu Glu Asn Leu Asn Ala Asp Asp Glu His Tyr Lys Ile Ile
 20 25 30
 Val Arg Asp Asn Lys Asp Ser Leu Leu Leu Lys Gln Ile Cys Gln His
 35 40 45
 Tyr Ala Gly Leu Asp Tyr Ile Ser Gly Gly Val Tyr Gly Phe Gly His
 50 55 60
 Asn Asn Asn Ile Ala Val Ala Tyr Val Lys Glu Lys Tyr Arg Pro Ala
 65 70 75 80
 Asp Asp Asp Tyr Ile Leu Phe Leu Asn Pro Asp Ile Ile Met Lys His
 85 90 95
 Asp Asp Leu Leu Thr Tyr Ile Lys Tyr Val Glu Ser Lys Arg Tyr Ala
 100 105 110
 Phe Ser Thr Leu Cys Leu Phe Arg Asp Glu Ala Lys Ser Leu His Asp
 115 120 125
 Tyr Ser Val Arg Lys Phe Pro Val Leu Ser Asp Phe Ile Val Ser Phe
 130 135 140
 Met Leu Gly Ile Lys Glu Gly Ala Asn Lys Ser Leu Ile
 145 150 155

<210> 375
 <211> 372
 <212> PRT
 <213> E. Coli

<400> 375
 Met Gly Lys Ser Ile Val Val Val Ser Ala Val Asn Phe Thr Thr Gly
 1 5 10 15
 Gly Pro Phe Thr Ile Leu Lys Lys Phe Leu Ala Ala Thr Asn Asn Lys
 20 25 30
 Glu Asn Val Ser Phe Ile Ala Leu Val His Ser Ala Lys Glu Leu Lys
 35 40 45
 Glu Ser Tyr Pro Trp Val Lys Phe Ile Glu Phe Pro Glu Val Lys Gly
 50 55 60
 Ser Trp Leu Lys Arg Leu His Phe Glu Tyr Val Val Cys Lys Lys Leu
 65 70 75 80
 Ser Lys Glu Leu Asn Ala Thr His Trp Ile Cys Leu His Asp Ile Thr
 85 90 95
 Ala Asn Val Val Thr Lys Lys Arg Tyr Val Tyr Cys His Asn Pro Ala
 100 105 110

Pro	Phe	Tyr	Lys	Gly	Ile	Leu	Phe	Arg	Glu	Ile	Leu	Met	Glu	Pro	Ser
	115						120					125			
Phe	Phe	Leu	Phe	Lys	Met	Leu	Tyr	Gly	Leu	Ile	Tyr	Lys	Ile	Asn	Ile
	130					135					140				
Lys	Lys	Asn	Thr	Ala	Val	Phe	Val	Gln	Gln	Phe	Trp	Met	Lys	Glu	Lys
145					150					155					160
Phe	Ile	Lys	Lys	Tyr	Ser	Ile	Asn	Asn	Ile	Ile	Val	Ser	Arg	Pro	Glu
				165					170					175	
Ile	Lys	Leu	Ser	Asp	Lys	Ser	Gln	Leu	Thr	Asp	Asp	Asp	Ser	Gln	Phe
			180					185					190		
Lys	Asn	Asn	Pro	Ser	Glu	Leu	Thr	Ile	Phe	Tyr	Pro	Ala	Val	Pro	Arg
		195					200					205			
Val	Phe	Lys	Asn	Tyr	Glu	Leu	Ile	Ile	Ser	Ala	Ala	Arg	Lys	Leu	Lys
	210					215					220				
Glu	Gln	Ser	Asn	Ile	Lys	Phe	Leu	Leu	Thr	Ile	Ser	Gly	Thr	Glu	Asn
225					230					235					240
Ala	Tyr	Ala	Lys	Tyr	Ile	Ile	Ser	Leu	Ala	Glu	Gly	Leu	Asp	Asn	Val
				245					250					255	
His	Phe	Leu	Gly	Tyr	Leu	Asp	Lys	Glu	Lys	Ile	Asp	His	Cys	Tyr	Asn
			260					265					270		
Ile	Ser	Asp	Ile	Val	Cys	Phe	Pro	Ser	Arg	Leu	Glu	Thr	Trp	Gly	Leu
		275					280					285			
Pro	Leu	Ser	Glu	Ala	Lys	Glu	Arg	Gly	Lys	Trp	Val	Leu	Ala	Ser	Asp
	290					295					300				
Phe	Pro	Phe	Thr	Arg	Glu	Thr	Leu	Gly	Ser	Tyr	Glu	Lys	Lys	Ala	Phe
305					310					315					320
Phe	Asp	Ser	Asn	Asn	Asp	Asp	Met	Leu	Val	Lys	Leu	Ile	Ile	Asp	Phe
				325					330					335	
Lys	Lys	Gly	Asn	Leu	Lys	Lys	Asp	Ile	Ser	Asp	Ala	Asn	Phe	Ile	Tyr
			340					345				350			
Arg	Asn	Glu	Asn	Val	Leu	Val	Gly	Phe	Asp	Glu	Leu	Val	Asn	Phe	Ile
		355					360					365			
Thr	Glu	Glu	His												
	370														

<210> 376

<211> 196

<212> PRT

<213> E. Coli

<400> 376

Met	Ile	Leu	Lys	Leu	Ala	Lys	Arg	Tyr	Gly	Leu	Cys	Gly	Phe	Ile	Arg
1				5					10					15	
Leu	Val	Arg	Asp	Val	Leu	Leu	Thr	Arg	Val	Phe	Tyr	Arg	Asn	Cys	Arg
			20					25					30		
Ile	Ile	Arg	Phe	Pro	Cys	Tyr	Ile	Arg	Asn	Asp	Gly	Ser	Ile	Asn	Phe
		35					40					45			
Gly	Glu	Asn	Phe	Thr	Ser	Gly	Val	Gly	Leu	Arg	Leu	Asp	Ala	Phe	Gly
	50					55					60				
Arg	Gly	Val	Ile	Phe	Phe	Ser	Asp	Asn	Val	Gln	Val	Asn	Asp	Tyr	Val
65					70					75					80
His	Ile	Ala	Ser	Ile	Glu	Ser	Val	Thr	Ile	Gly	Arg	Asp	Thr	Leu	Ile
			85						90					95	
Ala	Ser	Lys	Val	Phe	Ile	Thr	Asp	His	Asn	His	Gly	Ser	Phe	Lys	His
			100					105					110		
Ser	Asp	Pro	Met	Ser	Ser	Pro	Asn	Ile	Pro	Pro	Asp	Met	Arg	Thr	Leu

305 310 315 320
 Glu Glu Val Ile Asp Asp Leu Lys Thr Arg
 325 330

<210> 378
 <211> 388
 <212> PRT
 <213> E. Coli

<400> 378
 Met Ile Tyr Leu Val Ile Ser Val Phe Leu Ile Thr Ala Phe Ile Cys
 1 5 10 15
 Leu Tyr Leu Lys Lys Asp Ile Phe Tyr Pro Ala Val Cys Val Asn Ile
 20 25 30
 Ile Phe Ala Leu Val Leu Leu Gly Tyr Glu Ile Thr Ser Asp Ile Tyr
 35 40 45
 Ala Phe Gln Leu Asn Asp Ala Thr Leu Ile Phe Leu Leu Cys Asn Val
 50 55 60
 Leu Thr Phe Thr Leu Ser Cys Leu Leu Thr Glu Ser Val Leu Asp Leu
 65 70 75 80
 Asn Ile Arg Lys Val Asn Asn Ala Ile Tyr Ser Ile Pro Ser Lys Lys
 85 90 95
 Val His Asn Val Gly Leu Leu Val Ile Ser Phe Ser Met Ile Tyr Ile
 100 105 110
 Cys Met Arg Leu Ser Asn Tyr Gln Phe Gly Thr Ser Leu Leu Ser Tyr
 115 120 125
 Met Asn Leu Ile Arg Asp Ala Asp Val Glu Asp Thr Ser Arg Asn Phe
 130 135 140
 Ser Ala Tyr Met Gln Pro Ile Ile Leu Thr Thr Phe Ala Leu Phe Ile
 145 150 155 160
 Trp Ser Lys Lys Phe Thr Asn Thr Lys Val Ser Lys Thr Phe Thr Leu
 165 170 175
 Leu Val Phe Ile Val Phe Ile Phe Ala Ile Ile Leu Asn Thr Gly Lys
 180 185 190
 Gln Ile Val Phe Met Val Ile Ile Ser Tyr Ala Phe Ile Val Gly Val
 195 200 205
 Asn Arg Val Lys His Tyr Val Tyr Leu Ile Thr Ala Val Gly Val Leu
 210 215 220
 Phe Ser Leu Tyr Met Leu Phe Leu Arg Gly Leu Pro Gly Gly Met Ala
 225 230 235 240
 Tyr Tyr Leu Ser Met Tyr Leu Val Ser Pro Ile Ile Ala Phe Gln Glu
 245 250 255
 Phe Tyr Phe Gln Gln Val Ser Asn Ser Ala Ser Ser His Val Phe Trp
 260 265 270
 Phe Phe Glu Arg Leu Met Gly Leu Leu Thr Gly Gly Val Ser Met Ser
 275 280 285
 Leu His Lys Glu Phe Val Trp Val Gly Leu Pro Thr Asn Val Tyr Thr
 290 295 300
 Ala Phe Ser Asp Tyr Val Tyr Ile Ser Ala Glu Leu Ser Tyr Leu Met
 305 310 315 320
 Met Val Ile His Gly Cys Ile Ser Gly Val Leu Trp Arg Leu Ser Arg
 325 330 335
 Asn Tyr Ile Ser Val Lys Ile Phe Tyr Ser Tyr Phe Ile Tyr Thr Phe
 340 345 350
 Ser Phe Ile Phe Tyr His Glu Ser Phe Met Thr Asn Ile Ser Ser Trp
 355 360 365

Ile Gln Ile Thr Leu Cys Ile Ile Val Phe Ser Gln Phe Leu Lys Ala
 370 375 380
 Gln Lys Ile Lys
 385

<210> 379
 <211> 367
 <212> PRT
 <213> E. Coli

<400> 379
 Met Tyr Asp Tyr Ile Ile Val Gly Ser Gly Leu Phe Gly Ala Val Cys
 1 5 10 15
 Ala Asn Glu Leu Lys Lys Leu Asn Lys Lys Val Leu Val Ile Glu Lys
 20 25 30
 Arg Asn His Ile Gly Gly Asn Ala Tyr Thr Glu Asp Cys Glu Gly Ile
 35 40 45
 Gln Ile His Lys Tyr Gly Ala His Ile Phe His Thr Asn Asp Lys Tyr
 50 55 60
 Ile Trp Asp Tyr Val Asn Asp Leu Val Glu Phe Asn Arg Phe Thr Asn
 65 70 75 80
 Ser Pro Leu Ala Ile Tyr Lys Asp Lys Leu Phe Asn Leu Pro Phe Asn
 85 90 95
 Met Asn Thr Phe His Gln Met Trp Gly Val Lys Asp Pro Gln Glu Ala
 100 105 110
 Gln Asn Ile Ile Asn Ala Gln Lys Lys Tyr Gly Asp Lys Val Pro
 115 120 125
 Glu Asn Leu Glu Glu Gln Ala Ile Ser Leu Val Gly Glu Asp Leu Tyr
 130 135 140
 Gln Ala Leu Ile Lys Gly Tyr Thr Glu Lys Gln Trp Gly Arg Ser Ala
 145 150 155 160
 Lys Glu Leu Pro Ala Phe Ile Ile Lys Arg Ile Pro Val Arg Phe Thr
 165 170 175
 Phe Asp Asn Asn Tyr Phe Ser Asp Arg Tyr Gln Gly Ile Pro Val Gly
 180 185 190
 Gly Tyr Thr Lys Leu Ile Glu Lys Met Leu Glu Gly Val Asp Val Lys
 195 200 205
 Leu Gly Ile Asp Phe Leu Lys Asp Lys Asp Ser Leu Ala Ser Lys Ala
 210 215 220
 His Arg Ile Ile Tyr Thr Gly Pro Ile Asp Gln Tyr Phe Asp Tyr Arg
 225 230 235 240
 Phe Gly Ala Leu Glu Tyr Arg Ser Leu Lys Phe Glu Thr Glu Arg His
 245 250 255
 Glu Phe Pro Asn Phe Gln Gly Asn Ala Val Ile Asn Phe Thr Asp Ala
 260 265 270
 Asn Val Pro Tyr Thr Arg Ile Ile Glu His Lys His Phe Asp Tyr Val
 275 280 285
 Glu Thr Lys His Thr Val Val Thr Lys Glu Tyr Pro Leu Glu Trp Lys
 290 295 300
 Val Gly Asp Glu Pro Tyr Tyr Pro Val Asn Asp Asn Lys Asn Met Glu
 305 310 315 320
 Leu Phe Lys Lys Tyr Arg Glu Leu Ala Ser Arg Glu Asp Lys Val Ile
 325 330 335
 Phe Gly Gly Arg Leu Ala Glu Tyr Lys Tyr Tyr Asp Met His Gln Val
 340 345 350

Ile Ser Ala Ala Leu Tyr Gln Val Lys Asn Ile Met Ser Thr Asp
 355 360 365

<210> 380
 <211> 371
 <212> PRT
 <213> E. Coli

<400> 380
 Met Phe Pro Lys Ile Met Asn Asp Glu Asn Phe Phe Lys Lys Ala Ala
 1 5 10 15
 Ala His Gly Glu Glu Pro Pro Leu Thr Pro Gln Asn Glu His Gln Arg
 20 25 30
 Ser Gly Leu Arg Phe Ala Arg Arg Val Arg Leu Pro Arg Ala Val Gly
 35 40 45
 Leu Ala Gly Met Phe Leu Pro Ile Ala Ser Thr Leu Val Ser His Pro
 50 55 60
 Pro Pro Gly Trp Trp Trp Leu Val Leu Val Gly Trp Ala Phe Val Trp
 65 70 75 80
 Pro His Leu Ala Trp Gln Ile Ala Ser Arg Ala Val Asp Pro Leu Ser
 85 90 95
 Arg Glu Ile Tyr Asn Leu Lys Thr Asp Ala Val Leu Ala Gly Met Trp
 100 105 110
 Val Gly Val Met Gly Val Asn Val Leu Pro Ser Thr Ala Met Leu Met
 115 120 125
 Ile Met Cys Leu Asn Leu Met Gly Ala Gly Gly Pro Arg Leu Phe Val
 130 135 140
 Ala Gly Leu Val Leu Met Val Val Ser Cys Leu Val Thr Leu Glu Leu
 145 150 155 160
 Thr Gly Ile Thr Val Ser Phe Asn Ser Ala Pro Leu Glu Trp Trp Leu
 165 170 175
 Ser Leu Pro Ile Ile Val Ile Tyr Pro Leu Leu Phe Gly Trp Val Ser
 180 185 190
 Tyr Gln Thr Ala Thr Lys Leu Ala Glu His Lys Arg Arg Leu Gln Val
 195 200 205
 Met Ser Thr Arg Asp Gly Met Thr Gly Val Tyr Asn Arg Arg His Trp
 210 215 220
 Glu Thr Met Leu Arg Asn Glu Phe Asp Asn Cys Arg Arg His Asn Arg
 225 230 235 240
 Asp Ala Thr Leu Leu Ile Ile Asp Ile Asp His Phe Lys Ser Ile Asn
 245 250 255
 Asp Thr Trp Gly His Asp Val Gly Asp Glu Ala Ile Val Ala Leu Thr
 260 265 270
 Arg Gln Leu Gln Ile Thr Leu Arg Gly Ser Asp Val Ile Gly Arg Phe
 275 280 285
 Gly Gly Asp Glu Phe Ala Val Ile Met Ser Gly Thr Pro Ala Glu Ser
 290 295 300
 Ala Ile Thr Ala Met Leu Arg Val His Glu Gly Leu Asn Thr Leu Arg
 305 310 315 320
 Leu Pro Asn Thr Pro Gln Val Thr Leu Arg Ile Ser Val Gly Val Ala
 325 330 335
 Pro Leu Asn Pro Gln Met Ser His Tyr Arg Glu Trp Leu Lys Ser Ala
 340 345 350
 Asp Leu Ala Leu Tyr Lys Ala Lys Lys Ala Gly Arg Asn Arg Thr Glu
 355 360 365
 Val Ala Ala

370

<210> 381
 <211> 467
 <212> PRT
 <213> E. Coli

<400> 381
 Met Asp Val Asn Val Asp Gln Phe Asp Thr Glu Ala Phe Arg Thr Asp
 1 5 10 15
 Lys Leu Glu Leu Thr Ser Gly Asn Ile Ala Asp His Asn Gly Asn Val
 20 25 30
 Val Ser Gly Val Phe Asp Ile His Ser Ser Asp Tyr Val Leu Asn Ala
 35 40 45
 Asp Leu Val Asn Asp Arg Thr Trp Asp Thr Ser Lys Ser Asn Tyr Gly
 50 55 60
 Tyr Gly Ile Val Ala Met Asn Ser Asp Gly His Leu Thr Ile Asn Gly
 65 70 75 80
 Asn Gly Asp Val Asp Asn Gly Thr Glu Leu Asp Asn Ser Ser Val Asp
 85 90 95
 Asn Val Val Ala Ala Thr Gly Asn Tyr Lys Val Arg Ile Asp Asn Ala
 100 105 110
 Thr Gly Ala Gly Ala Ile Ala Asp Tyr Lys Asp Lys Glu Ile Ile Tyr
 115 120 125
 Val Asn Asp Val Asn Ser Asn Ala Thr Phe Ser Ala Ala Asn Lys Ala
 130 135 140
 Asp Leu Gly Ala Tyr Thr Tyr Gln Ala Glu Gln Arg Gly Asn Thr Val
 145 150 155 160
 Val Leu Gln Gln Met Glu Leu Thr Asp Tyr Ala Asn Met Ala Leu Ser
 165 170 175
 Ile Pro Ser Ala Asn Thr Asn Ile Trp Asn Leu Glu Gln Asp Thr Val
 180 185 190
 Gly Thr Arg Leu Thr Asn Ser Arg His Gly Leu Ala Asp Asn Gly Gly
 195 200 205
 Ala Trp Val Ser Tyr Phe Gly Gly Asn Phe Asn Gly Asp Asn Gly Thr
 210 215 220
 Ile Asn Tyr Asp Gln Asp Val Asn Gly Ile Met Val Gly Val Asp Thr
 225 230 235 240
 Lys Ile Asp Gly Asn Asn Ala Lys Trp Ile Val Gly Ala Ala Ala Gly
 245 250 255
 Phe Ala Lys Gly Asp Met Asn Asp Arg Ser Gly Gln Val Asp Gln Asp
 260 265 270
 Ser Gln Thr Ala Tyr Ile Tyr Ser Ser Ala His Phe Ala Asn Asn Val
 275 280 285
 Phe Val Asp Gly Ser Leu Ser Tyr Ser His Phe Asn Asn Asp Leu Ser
 290 295 300
 Ala Thr Met Ser Asn Gly Thr Tyr Val Asp Gly Ser Thr Asn Ser Asp
 305 310 315 320
 Ala Trp Gly Phe Gly Leu Lys Ala Gly Tyr Asp Phe Lys Leu Gly Asp
 325 330 335
 Ala Gly Tyr Val Thr Pro Tyr Gly Ser Val Ser Gly Leu Phe Gln Ser
 340 345 350
 Gly Asp Asp Tyr Gln Leu Ser Asn Asp Met Lys Val Asp Gly Gln Ser
 355 360 365
 Tyr Asp Ser Met Arg Tyr Glu Leu Gly Val Asp Ala Gly Tyr Thr Phe
 370 375 380
 Thr Tyr Ser Glu Asp Gln Ala Leu Thr Pro Tyr Phe Lys Leu Ala Tyr

385 390 395 400
 Val Tyr Asp Asp Ser Asn Asn Asp Asn Asp Val Asn Gly Asp Ser Ile
 405 410 415
 Asp Asn Gly Thr Glu Gly Ser Ala Val Arg Val Gly Leu Gly Thr Gln
 420 425 430
 Phe Ser Phe Thr Lys Asn Phe Ser Ala Tyr Thr Asp Ala Asn Tyr Leu
 435 440 445
 Gly Gly Gly Asp Val Asp Gln Asp Trp Ser Ala Asn Val Gly Val Lys
 450 455 460
 Tyr Thr Trp
 465

<210> 382
 <211> 222
 <212> PRT
 <213> E. Coli

<400> 382
 Met Pro Val Lys Asp Leu Thr Gly Ile Thr Ala Lys Asp Ala Gln Met
 1 5 10 15
 Leu Ser Val Val Lys Pro Leu Gln Glu Phe Gly Lys Leu Asp Lys Cys
 20 25 30
 Leu Ser Arg Tyr Gly Thr Arg Phe Glu Phe Asn Asn Glu Lys Gln Val
 35 40 45
 Ile Phe Ser Ser Asp Val Asn Asn Glu Asp Thr Phe Val Ile Leu Glu
 50 55 60
 Gly Val Ile Ser Leu Arg Arg Glu Glu Asn Val Leu Ile Gly Ile Thr
 65 70 75 80
 Gln Ala Pro Tyr Ile Met Gly Leu Ala Asp Gly Leu Met Lys Asn Asp
 85 90 95
 Ile Pro Tyr Lys Leu Ile Ser Glu Gly Asn Cys Thr Gly Tyr His Leu
 100 105 110
 Pro Ala Lys Gln Thr Ile Thr Leu Ile Glu Gln Asn Gln Leu Trp Arg
 115 120 125
 Asp Ala Phe Tyr Trp Leu Ala Trp Gln Asn Arg Ile Leu Glu Leu Arg
 130 135 140
 Asp Val Gln Leu Ile Gly His Asn Ser Tyr Glu Gln Ile Arg Ala Thr
 145 150 155 160
 Leu Leu Ser Met Ile Asp Trp Asn Glu Glu Leu Arg Ser Arg Ile Gly
 165 170 175
 Val Met Asn Tyr Ile His Gln Arg Thr Arg Ile Ser Arg Ser Val Val
 180 185 190
 Ala Glu Val Leu Ala Ala Leu Arg Lys Gly Gly Tyr Ile Glu Met Asn
 195 200 205
 Lys Gly Lys Leu Val Ala Ile Asn Arg Leu Pro Ser Glu Tyr
 210 215 220

<210> 383
 <211> 84
 <212> PRT
 <213> E. Coli

<400> 383
 Met Thr Asp Lys Ile Arg Thr Leu Gln Gly Arg Val Val Ser Asp Lys

1		5		10		15
Met	Glu	Lys	Ser	Ile	Val	Val
		20		25		30
Ile	Tyr	Gly	Lys	Phe	Ile	Lys
	35		40		45	
Glu	Asn	Asn	Glu	Cys	Gly	Ile
	50		55		60	
Arg	Pro	Leu	Ser	Lys	Thr	Lys
65		70		75		80
Lys	Ala	Val	Leu			

<210> 384
 <211> 63
 <212> PRT
 <213> E. Coli

<400> 384															
Met	Lys	Ala	Lys	Glu	Leu	Arg	Glu	Lys	Ser	Val	Glu	Glu	Leu	Asn	Thr
1			5				10						15		
Glu	Leu	Leu	Asn	Leu	Leu	Arg	Glu	Gln	Phe	Asn	Leu	Arg	Met	Gln	Ala
		20					25					30			
Ala	Ser	Gly	Gln	Leu	Gln	Gln	Ser	His	Leu	Leu	Lys	Gln	Val	Arg	Arg
	35				40						45				
Asp	Val	Ala	Arg	Val	Lys	Thr	Leu	Leu	Asn	Glu	Lys	Ala	Gly	Ala	
	50				55						60				

<210> 385
 <211> 136
 <212> PRT
 <213> E. Coli

<400> 385															
Met	Leu	Gln	Pro	Lys	Arg	Thr	Lys	Phe	Arg	Lys	Met	His	Lys	Gly	Arg
1			5				10						15		
Asn	Arg	Gly	Leu	Ala	Gln	Gly	Thr	Asp	Val	Ser	Phe	Gly	Ser	Phe	Gly
	20						25					30			
Leu	Lys	Ala	Val	Gly	Arg	Gly	Arg	Leu	Thr	Ala	Arg	Gln	Ile	Glu	Ala
	35				40						45				
Ala	Arg	Arg	Ala	Met	Thr	Arg	Ala	Val	Lys	Arg	Gln	Gly	Lys	Ile	Trp
	50				55					60					
Ile	Arg	Val	Phe	Pro	Asp	Lys	Pro	Ile	Thr	Glu	Lys	Pro	Leu	Ala	Val
65			70						75					80	
Arg	Met	Gly	Lys	Gly	Lys	Gly	Asn	Val	Glu	Tyr	Trp	Val	Ala	Leu	Ile
			85				90						95		
Gln	Pro	Gly	Lys	Val	Leu	Tyr	Glu	Met	Asp	Gly	Val	Pro	Glu	Glu	Leu
	100						105					110			
Ala	Arg	Glu	Ala	Phe	Lys	Leu	Ala	Ala	Ala	Lys	Leu	Pro	Ile	Lys	Thr
	115					120						125			
Thr	Phe	Val	Thr	Lys	Thr	Val	Met								
	130					135									

<210> 386
 <211> 233

<212> PRT
 <213> E. Coli

<400> 386
 Met Gly Gln Lys Val His Pro Asn Gly Ile Arg Leu Gly Ile Val Lys
 1 5 10 15
 Pro Trp Asn Ser Thr Trp Phe Ala Asn Thr Lys Glu Phe Ala Asp Asn
 20 25 30
 Leu Asp Ser Asp Phe Lys Val Arg Gln Tyr Leu Thr Lys Glu Leu Ala
 35 40 45
 Lys Ala Ser Val Ser Arg Ile Val Ile Glu Arg Pro Ala Lys Ser Ile
 50 55 60
 Arg Val Thr Ile His Thr Ala Arg Pro Gly Ile Val Ile Gly Lys Lys
 65 70 75 80
 Gly Glu Asp Val Glu Lys Leu Arg Lys Val Val Ala Asp Ile Ala Gly
 85 90 95
 Val Pro Ala Gln Ile Asn Ile Ala Glu Val Arg Lys Pro Glu Leu Asp
 100 105 110
 Ala Lys Leu Val Ala Asp Ser Ile Thr Ser Gln Leu Glu Arg Arg Val
 115 120 125
 Met Phe Arg Arg Ala Met Lys Arg Ala Val Gln Asn Ala Met Arg Leu
 130 135 140
 Gly Ala Lys Gly Ile Lys Val Glu Val Ser Gly Arg Leu Gly Gly Ala
 145 150 155 160
 Glu Ile Ala Arg Thr Glu Trp Tyr Arg Glu Gly Arg Val Pro Leu His
 165 170 175
 Thr Leu Arg Ala Asp Ile Asp Tyr Asn Thr Ser Glu Ala His Thr Thr
 180 185 190
 Tyr Gly Val Ile Gly Val Lys Val Trp Ile Phe Lys Gly Glu Ile Leu
 195 200 205
 Gly Gly Met Ala Ala Val Glu Gln Pro Glu Lys Pro Ala Ala Gln Pro
 210 215 220
 Lys Lys Gln Gln Arg Lys Gly Arg Lys
 225 230

<210> 387
 <211> 110
 <212> PRT
 <213> E. Coli

<400> 387
 Met Glu Thr Ile Ala Lys His Arg His Ala Arg Ser Ser Ala Gln Lys
 1 5 10 15
 Val Arg Leu Val Ala Asp Leu Ile Arg Gly Lys Lys Val Ser Gln Ala
 20 25 30
 Leu Asp Ile Leu Thr Tyr Thr Asn Lys Lys Ala Ala Val Leu Val Lys
 35 40 45
 Lys Val Leu Glu Ser Ala Ile Ala Asn Ala Glu His Asn Asp Gly Ala
 50 55 60
 Asp Ile Asp Asp Leu Lys Val Thr Lys Ile Phe Val Asp Glu Gly Pro
 65 70 75 80
 Ser Met Lys Arg Ile Met Pro Arg Ala Lys Gly Arg Ala Asp Arg Ile
 85 90 95
 Leu Lys Arg Thr Ser His Ile Thr Val Val Ser Asp Arg
 100 105 110

<210> 388
 <211> 92
 <212> PRT
 <213> E. Coli

<400> 388
 Met Pro Arg Ser Leu Lys Lys Gly Pro Phe Ile Asp Leu His Leu Leu
 1 5 10 15
 Met Lys Val Glu Lys Ala Val Glu Ser Gly Asp Lys Lys Pro Leu Arg
 20 25 30
 Thr Trp Ser Arg Arg Ser Thr Ile Phe Pro Asn Met Ile Gly Leu Thr
 35 40 45
 Ile Ala Val His Asn Gly Arg Gln His Val Pro Val Phe Val Thr Asp
 50 55 60
 Glu Met Val Gly His Lys Leu Gly Glu Phe Ala Pro Thr Arg Thr Tyr
 65 70 75 80
 Arg Gly His Ala Ala Asp Lys Lys Ala Lys Lys Lys
 85 90

<210> 389
 <211> 273
 <212> PRT
 <213> E. Coli

<400> 389
 Met Ala Val Val Lys Cys Lys Pro Thr Ser Pro Gly Arg Arg His Val
 1 5 10 15
 Val Lys Val Val Asn Pro Glu Leu His Lys Gly Lys Pro Phe Ala Pro
 20 25 30
 Leu Leu Glu Lys Asn Ser Lys Ser Gly Gly Arg Asn Asn Asn Gly Arg
 35 40 45
 Ile Thr Thr Arg His Ile Gly Gly Gly His Lys Gln Ala Tyr Arg Ile
 50 55 60
 Val Asp Phe Lys Arg Asn Lys Asp Gly Ile Pro Ala Val Val Glu Arg
 65 70 75 80
 Leu Glu Tyr Asp Pro Asn Arg Ser Ala Asn Ile Ala Leu Val Leu Tyr
 85 90 95
 Lys Asp Gly Glu Arg Arg Tyr Ile Leu Ala Pro Lys Gly Leu Lys Ala
 100 105 110
 Gly Asp Gln Ile Gln Ser Gly Val Asp Ala Ala Ile Lys Pro Gly Asn
 115 120 125
 Thr Leu Pro Met Arg Asn Ile Pro Val Gly Ser Thr Val His Asn Val
 130 135 140
 Glu Met Lys Pro Gly Lys Gly Gly Gln Leu Ala Arg Ser Ala Gly Thr
 145 150 155 160
 Tyr Val Gln Ile Val Ala Arg Asp Gly Ala Tyr Val Thr Leu Arg Leu
 165 170 175
 Arg Ser Gly Glu Met Arg Lys Val Glu Ala Asp Cys Arg Ala Thr Leu
 180 185 190
 Gly Glu Val Gly Asn Ala Glu His Met Leu Arg Val Leu Gly Lys Ala
 195 200 205
 Gly Ala Ala Arg Trp Arg Gly Val Arg Pro Thr Val Arg Gly Thr Ala

210	215	220
Met Asn Pro Val Asp His	Pro His Gly Gly Gly	Glu Gly Arg Asn Phe
225	230	235
Gly Lys His Pro Val Thr	Pro Trp Gly Val Gln Thr	Lys Gly Lys Lys
245	250	255
Thr Arg Ser Asn Lys Arg Thr	Asp Lys Phe Ile Val Arg	Arg Arg Ser
260	265	270
Lys		

<210> 390
 <211> 100
 <212> PRT
 <213> E. Coli

<400> 390
Met Ile Arg Glu Glu Arg Leu Leu Lys Val Leu Arg Ala Pro His Val
1 5 10 15
Ser Glu Lys Ala Ser Thr Ala Met Glu Lys Ser Asn Thr Ile Val Leu
20 25 30
Lys Val Ala Lys Asp Ala Thr Lys Ala Glu Ile Lys Ala Ala Val Gln
35 40 45
Lys Leu Phe Glu Val Glu Val Glu Val Val Asn Thr Leu Val Val Lys
50 55 60
Gly Lys Val Lys Arg His Gly Gln Arg Ile Gly Arg Arg Ser Asp Trp
65 70 75 80
Lys Lys Ala Tyr Val Thr Leu Lys Glu Gly Gln Asn Leu Asp Phe Val
85 90 95
Gly Gly Ala Glu
100

<210> 391
 <211> 201
 <212> PRT
 <213> E. Coli

<400> 391
Met Glu Leu Val Leu Lys Asp Ala Gln Ser Ala Leu Thr Val Ser Glu
1 5 10 15
Thr Thr Phe Gly Arg Asp Phe Asn Glu Ala Leu Val His Gln Val Val
20 25 30
Val Ala Tyr Ala Ala Gly Ala Arg Gln Gly Thr Arg Ala Gln Lys Thr
35 40 45
Arg Ala Glu Val Thr Gly Ser Gly Lys Lys Pro Trp Arg Gln Lys Gly
50 55 60
Thr Gly Arg Ala Arg Ser Gly Ser Ile Lys Ser Pro Ile Trp Arg Ser
65 70 75 80
Gly Gly Val Thr Phe Ala Ala Arg Pro Gln Asp His Ser Gln Lys Val
85 90 95
Asn Lys Lys Met Tyr Arg Gly Ala Leu Lys Ser Ile Leu Ser Glu Leu
100 105 110
Val Arg Gln Asp Arg Leu Ile Val Val Glu Lys Phe Ser Val Glu Ala
115 120 125

Pro Lys Thr Lys Leu Leu Ala Gln Lys Leu Lys Asp Met Ala Leu Glu
 130 135 140
 Asp Val Leu Ile Ile Thr Gly Glu Leu Asp Glu Asn Leu Phe Leu Ala
 145 150 155 160
 Ala Arg Asn Leu His Lys Val Asp Val Arg Asp Ala Thr Gly Ile Asp
 165 170 175
 Pro Val Ser Leu Ile Ala Phe Asp Lys Val Val Met Thr Ala Asp Ala
 180 185 190
 Val Lys Gln Val Glu Glu Met Leu Ala
 195 200

<210> 392
 <211> 209
 <212> PRT
 <213> E. Coli

<400> 392
 Met Ile Gly Leu Val Gly Lys Lys Val Gly Met Thr Arg Ile Phe Thr
 1 5 10 15
 Glu Asp Gly Val Ser Ile Pro Val Thr Val Ile Glu Val Glu Ala Asn
 20 25 30
 Arg Val Thr Gln Val Lys Asp Leu Ala Asn Asp Gly Tyr Arg Ala Ile
 35 40 45
 Gln Val Thr Thr Gly Ala Lys Lys Ala Asn Arg Val Thr Lys Pro Glu
 50 55 60
 Ala Gly His Phe Ala Lys Ala Gly Val Glu Ala Gly Arg Gly Leu Trp
 65 70 75 80
 Glu Phe Arg Leu Ala Glu Gly Glu Glu Phe Thr Val Gly Gln Ser Ile
 85 90 95
 Ser Val Glu Leu Phe Ala Asp Val Lys Lys Val Asp Val Thr Gly Thr
 100 105 110
 Ser Lys Gly Lys Gly Phe Ala Gly Thr Val Lys Arg Trp Asn Phe Arg
 115 120 125
 Thr Gln Asp Ala Thr His Gly Asn Ser Leu Ser His Arg Val Pro Gly
 130 135 140
 Ser Ile Gly Gln Asn Gln Thr Pro Gly Lys Val Phe Lys Gly Lys Lys
 145 150 155 160
 Met Ala Gly Gln Met Gly Asn Glu Arg Val Thr Val Gln Ser Leu Asp
 165 170 175
 Val Val Arg Val Asp Ala Glu Arg Asn Leu Leu Leu Val Lys Gly Ala
 180 185 190
 Val Pro Gly Ala Thr Gly Ser Asp Leu Ile Val Lys Pro Ala Val Lys
 195 200 205
 Ala

<210> 393
 <211> 103
 <212> PRT
 <213> E. Coli

<400> 393
 Met Gln Asn Gln Arg Ile Arg Ile Arg Leu Lys Ala Phe Asp His Arg

1	5	10	15
Leu Ile Asp	Gln Ala Thr Ala Glu	Ile Val Glu Thr Ala Lys Arg Thr	
	20	25	30
Gly Ala Gln	Val Arg Gly Pro Ile	Pro Leu Pro Thr Arg Lys Glu Arg	
	35	40	45
Phe Thr Val	Leu Ile Ser Pro His Val Asn Lys Asp	Ala Arg Asp Gln	
	50	55	60
Tyr Glu Ile	Arg Thr His Leu Arg Leu Val Asp	Ile Val Glu Pro Thr	
	65	70	75
Glu Lys Thr	Val Asp Ala Leu Met Arg Leu Asp	Leu Ala Ala Gly Val	
	85	90	95
Asp Val Gln	Ile Ser Leu Gly		
	100		

<210> 394
 <211> 118
 <212> PRT
 <213> E. Coli

<400> 394															
Met Ala Arg	Val Lys Arg	Gly Val Ile	Ala Arg Ala Arg	His Lys Lys											
1	5	10	15												
Ile Leu Lys	Gln Ala Lys Gly Tyr Tyr	Gly Ala Arg Ser Arg	Val Tyr												
	20	25	30												
Arg Val Ala	Phe Gln Ala Val Ile Lys	Ala Gly Gln Tyr Ala Tyr Arg													
	35	40	45												
Asp Arg Arg	Gln Arg Lys Arg Gln Phe Arg	Gln Leu Trp Ile Ala Arg													
	50	55	60												
Ile Asn Ala	Ala Ala Arg Gln Asn Gly Ile Ser Tyr	Ser Lys Phe Ile													
	65	70	75												
Asn Gly Leu	Lys Lys Ala Ser Val Glu Ile Asp	Arg Lys Ile Leu Ala													
	85	90	95												
Asp Ile Ala	Val Phe Asp Lys Val Ala Phe Thr	Ala Leu Val Glu Lys													
	100	105	110												
Ala Lys Ala	Ala Leu Ala														
	115														

<210> 395
 <211> 65
 <212> PRT
 <213> E. Coli

<400> 395															
Met Pro Lys	Ile Lys Thr Val Arg Gly	Ala Ala Lys Arg Phe Lys Lys													
1	5	10	15												
Thr Gly Lys	Gly Gly Phe Lys His Lys His	Ala Asn Leu Arg His Ile													
	20	25	30												
Leu Thr Lys	Lys Ala Thr Lys Arg Lys Arg	His Leu Arg Pro Lys Ala													
	35	40	45												
Met Val Ser	Lys Gly Asp Leu Gly Leu Val Ile	Ala Cys Leu Pro Tyr													
	50	55	60												
Ala															
65															

<210> 396
 <211> 180
 <212> PRT
 <213> E. Coli

<400> 396
 Met Lys Gly Gly Lys Arg Val Gln Thr Ala Arg Pro Asn Arg Ile Asn
 1 5 10 15
 Gly Glu Ile Arg Ala Gln Glu Val Arg Leu Thr Gly Leu Glu Gly Glu
 20 25 30
 Gln Leu Gly Ile Val Ser Leu Arg Glu Ala Leu Glu Lys Ala Glu Glu
 35 40 45
 Ala Gly Val Asp Leu Val Glu Ile Ser Pro Asn Ala Glu Pro Pro Val
 50 55 60
 Cys Arg Ile Met Asp Tyr Gly Lys Phe Leu Tyr Glu Lys Ser Lys Ser
 65 70 75 80
 Ser Lys Glu Gln Lys Lys Lys Gln Lys Val Ile Gln Val Lys Glu Ile
 85 90 95
 Lys Phe Arg Pro Gly Thr Asp Glu Gly Asp Tyr Gln Val Lys Leu Arg
 100 105 110
 Ser Leu Ile Arg Phe Leu Glu Glu Gly Asp Lys Ala Lys Ile Thr Leu
 115 120 125
 Arg Phe Arg Gly Arg Glu Met Ala His Gln Gln Ile Gly Met Glu Val
 130 135 140
 Leu Asn Arg Val Lys Asp Asp Leu Gln Glu Leu Ala Val Val Glu Ser
 145 150 155 160
 Phe Pro Thr Lys Ile Glu Gly Arg Gln Met Ile Met Val Leu Ala Pro
 165 170 175
 Lys Lys Lys Gln
 180

<210> 397
 <211> 642
 <212> PRT
 <213> E. Coli

<400> 397
 Met Pro Val Ile Thr Leu Pro Asp Gly Ser Gln Arg His Tyr Asp His
 1 5 10 15
 Ala Val Ser Pro Met Asp Val Ala Leu Asp Ile Gly Pro Gly Leu Ala
 20 25 30
 Lys Ala Cys Ile Ala Gly Arg Val Asn Gly Glu Leu Val Asp Ala Cys
 35 40 45
 Asp Leu Ile Glu Asn Asp Ala Gln Leu Ser Ile Ile Thr Ala Lys Asp
 50 55 60
 Glu Glu Gly Leu Glu Ile Ile Arg His Ser Cys Ala His Leu Leu Gly
 65 70 75 80
 His Ala Ile Lys Gln Leu Trp Pro His Thr Lys Met Ala Ile Gly Pro
 85 90 95
 Val Ile Asp Asn Gly Phe Tyr Tyr Asp Val Asp Leu Asp Arg Thr Leu
 100 105 110
 Thr Gln Glu Asp Val Glu Ala Leu Glu Lys Arg Met His Glu Leu Ala
 115 120 125

Glu	Lys	Asn	Tyr	Asp	Val	Ile	Lys	Lys	Lys	Val	Ser	Trp	His	Glu	Ala
130						135					140				
Arg	Glu	Thr	Phe	Ala	Asn	Arg	Gly	Glu	Ser	Tyr	Lys	Val	Ser	Ile	Leu
145					150					155					160
Asp	Glu	Asn	Ile	Ala	His	Asp	Asp	Lys	Pro	Gly	Leu	Tyr	Phe	His	Glu
				165					170					175	
Glu	Tyr	Val	Asp	Met	Cys	Arg	Gly	Pro	His	Val	Pro	Asn	Met	Arg	Phe
			180					185					190		
Cys	His	His	Phe	Lys	Leu	Met	Lys	Thr	Ala	Gly	Ala	Tyr	Trp	Arg	Gly
		195					200					205			
Asp	Ser	Asn	Asn	Lys	Met	Leu	Gln	Arg	Ile	Tyr	Gly	Thr	Ala	Trp	Ala
	210					215					220				
Asp	Lys	Lys	Ala	Leu	Asn	Ala	Tyr	Leu	Gln	Arg	Leu	Glu	Glu	Ala	Ala
225					230					235					240
Lys	Arg	Asp	His	Arg	Lys	Ile	Gly	Lys	Gln	Leu	Asp	Leu	Tyr	His	Met
				245					250					255	
Gln	Glu	Glu	Ala	Pro	Gly	Met	Val	Phe	Trp	His	Asn	Asp	Gly	Trp	Thr
			260					265					270		
Ile	Phe	Arg	Glu	Leu	Glu	Val	Phe	Val	Arg	Ser	Lys	Leu	Lys	Glu	Tyr
		275					280					285			
Gln	Tyr	Gln	Glu	Val	Lys	Gly	Pro	Phe	Met	Met	Asp	Arg	Val	Leu	Trp
	290					295					300				
Glu	Lys	Thr	Gly	His	Trp	Asp	Asn	Tyr	Lys	Asp	Ala	Met	Phe	Thr	Thr
305					310					315					320
Ser	Ser	Glu	Asn	Arg	Glu	Tyr	Cys	Ile	Lys	Pro	Met	Asn	Cys	Pro	Gly
				325					330					335	
His	Val	Gln	Ile	Phe	Asn	Gln	Gly	Leu	Lys	Ser	Tyr	Arg	Asp	Leu	Pro
			340					345					350		
Leu	Arg	Met	Ala	Glu	Phe	Gly	Ser	Cys	His	Arg	Asn	Glu	Pro	Ser	Gly
		355					360					365			
Ser	Leu	His	Gly	Leu	Met	Arg	Val	Arg	Gly	Phe	Thr	Gln	Asp	Asp	Ala
	370					375					380				
His	Ile	Phe	Cys	Thr	Glu	Glu	Gln	Ile	Arg	Asp	Glu	Val	Asn	Gly	Cys
385					390					395					400
Ile	Arg	Leu	Val	Tyr	Asp	Met	Tyr	Ser	Thr	Phe	Gly	Phe	Glu	Lys	Ile
				405					410					415	
Val	Val	Lys	Leu	Ser	Thr	Arg	Pro	Glu	Lys	Arg	Ile	Gly	Ser	Asp	Glu
			420					425					430		
Met	Trp	Asp	Arg	Ala	Glu	Ala	Asp	Leu	Ala	Val	Ala	Leu	Glu	Glu	Asn
		435					440					445			
Asn	Ile	Pro	Phe	Glu	Tyr	Gln	Leu	Gly	Glu	Gly	Ala	Phe	Tyr	Gly	Pro
	450					455					460				
Lys	Ile	Glu	Phe	Thr	Leu	Tyr	Asp	Cys	Leu	Asp	Arg	Ala	Trp	Gln	Cys
465					470					475					480
Gly	Thr	Val	Gln	Leu	Asp	Phe	Ser	Leu	Pro	Ser	Arg	Leu	Ser	Ala	Ser
				485					490					495	
Tyr	Val	Gly	Glu	Asp	Asn	Glu	Arg	Lys	Val	Pro	Val	Met	Ile	His	Arg
			500					505					510		
Ala	Ile	Leu	Gly	Ser	Met	Glu	Arg	Phe	Ile	Gly	Ile	Leu	Thr	Glu	Glu
		515					520					525			
Phe	Ala	Gly	Phe	Phe	Pro	Thr	Trp	Leu	Ala	Pro	Val	Gln	Val	Val	Ile
	530					535					540				
Met	Asn	Ile	Thr	Asp	Ser	Gln	Ser	Glu	Tyr	Val	Asn	Glu	Leu	Thr	Gln
545					550					555					560
Lys	Leu	Ser	Asn	Ala	Gly	Ile	Arg	Val	Lys	Ala	Asp	Leu	Arg	Asn	Glu
				565					570					575	
Lys	Ile	Gly	Phe	Lys	Ile	Arg	Glu	His	Thr	Leu	Arg	Arg	Val	Pro	Tyr

gugagcuauu	acgcuuucuu	uaaaugaugg	cugcuucuaa	gccaaacaucc	uggcugucug	1860
ggccuuccca	caucguuucc	cacuaaacca	ugacuunggg	accuuagcug	gcgguucuggg	1920
uuguuucccu	cuucacgacg	gacguuagca	cccgccgugu	gucucccgug	auaacauucu	1980
ccgguaauucg	caguungcau	cggguuggua	agucgggaug	accccuugc	cgaaacagug	2040
cucuaccccc	ggagaugaau	ucacgaggcg	cuaccuaaa	agcuuucggg	gagaaccagc	2100
uauucuccgg	uuugauuggc	cuuucacccc	cagccacaag	ucauccgcua	auuuuuaac	2160
auuagucggg	ucgguccucc	aguuaugugu	acccaaccuu	caaccugccc	auggcuaugu	2220
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uuagauguuu	caguuccccc	gguucgccuc	auuaaccuau	ggauucaguu	aaugauagug	2760
ugucgaaaca	cacuggguuu	ccccauucgg	aaaucgccgg	uuauaacggg	ucauauacc	2820
uuaccgacgc	uuauccgaga	uuagcacguc	cuucaucgcc	ucugacugcc	agggcaucca	2880
ccguguacgc	uuagucgcuu	aacc				2904

<210> 400

<211> 120

<212> RNA

<213> E. Coli

<400> 400

augccuggca	guucccuacu	cucgcauggg	gagaccccac	acuaccaucg	gcgcuacggc	60
guuucacuuc	ugaguucggc	auggggucag	gugggaccac	cgcgcuacgg	ccgccaggca	120

<210> 401

<211> 76

<212> RNA

<213> E. Coli

<400> 401

gucccuucg	ucuagaggcc	caggacaccg	cccuuucacg	gcgguaacag	ggguucgaau	60
cccuagggg	acgccca					76

<210> 402

<211> 1549

<212> RNA

<213> E. Coli

<400> 402

aaaugaaga	guuugaucuu	ggcucagauu	gaacgcuggc	ggcaggccua	acacaugcaa	60
gucgaacggg	aacaggaagc	agcuugcugc	uucgcugacg	aguggcgagc	gggugaguua	120
ugucugggaa	gcugccugau	ggaggggggu	aacuacugga	aacgguagcu	aaauaccgcau	180
aaugucgcaa	gaccaaagag	ggggaccuuc	gggccucuuu	ccaucggauu	ugcccagauu	240
ggauuagcuu	guuggugggg	uaacggcuca	ccaaggcgac	gaucuuuagc	uggucugaga	300
ggauagaccg	ccacacugga	acugagacac	gguccagacu	ccuacgggag	gcagcagugg	360
ggauauuugc	acaauggggc	caagccugau	gcagccauug	cgcguguaug	aagaaggccu	420

ucggguugua	aaguacuuuc	agcggggagg	aagggaguua	aguuaauacc	uuugcucauu	480
gacguuaccc	gcagaagaag	caccggcuua	cuccgugcca	gcagccgcgg	uaauacggag	540
ggugcaagcg	uuaaucggaa	uuacugggcg	uaaagcgcac	gcaggcgggg	ugguuaaguc	600
agaugugaaa	uccccgggcu	caaccuggga	acugcaucug	auacuggcaa	gcuugagucu	660
cguagagggg	gguagaauuc	cagguguagc	ggugaaaugc	guagagauuc	ggaggaauac	720
cgguggcgaa	ggcggcccc	uggacgaaga	cugacgcuca	ggugcgaaag	cguggggagc	780
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ccuugaggcg	uggcuuccgg	agcuaacgcg	uuaagucgac	cgccugggga	guacggccgc	900
aagguuaaaa	cucaaaugaa	uugacggggg	cccgcacaag	cgguggagca	ugugguuuaa	960
uucgaugcaa	cgcgaagaac	cuuaccuggu	cuugacaucc	acggaaguuu	ucagagauga	1020
gaugugccu	ucgggaaccg	ugagacaggu	gcugcauggc	ugucgucagc	ucguguugug	1080
aaauuguggg	uuaagucccg	caacgagcgc	aaccuuuauc	cuuuguugcc	agcgguccgg	1140
ccgggaacuc	aaaggagacu	gccagugaua	aacuggagga	agguggggau	gacgucaagu	1200
caucauggcc	cuuacgacca	gggcuacaca	cgugcuacaa	uggcgcauac	aaagagaagc	1260
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<210> 403

<211> 17

<212> DNA

<213> Artificial

<220>

<223> Primer Oligonucleotide

<400> 403

tgtttatcag accgctt

17

<210> 404

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Primer Oligonucleotide

<400> 404

acaatttcac acagcctc

18

<210> 405

<211> 159

<212> DNA

<213> Escherichia coli

<400> 405

caggtggtat ggaaacccaa aatggagacg ggaagctgaa ccagatagtt actggaggtg

60

atcaccagca gatgaaataa cgataaccag aacaacgcct tatagcggtg agtttgcgag

120

aaaacgttca tattgtacct ttttgattaa ccattgggg

159

<210> 406

<211> 640

<212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(640)
 <223> n = A,T,C or G

<400> 406
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 aaaaaaggc ggggatttgt nagccacggg ngattanttt anaataaatt aagtgttgcc 120
 ataaggggac aaagngaagg aagtggntat taanggannc gccaatgcga nttagggcag 180
 accattcggc cattcgcctt cttggttata gaagttcata cagatagccg ttgccngacc 240
 gaccagattc gcttcnggca caaagcccca gtaacggctg tccgcgctgt tgcgcgggtt 300
 gtcgcccata atgaagtatt gtcccggagg aacaatccag gttgccagtt gttgccctgg 360
 ctgctggtaa tacatcccca cctgatacctg cgcaatcggc actgtcagaa tgcgggtgcgt 420
 cacatcaccc agtgtctctt tacgctcgga aagacgaatt ccattttctt tggtttcggt 480
 tttcggcact tcaaagaatc cgctggctgc tccccacca ttacggcgtg agaaggtctg 540
 aacgaaatcg ctcggttcca cgtttgagta ggtgaccggc agcgcgtttt cacacgcctg 600
 gccggaactg catcccgggt gaatcgtcag ctcttttgag . 640

<210> 407
 <211> 682
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(682)
 <223> n = A,T,C or G

<400> 407
 cctgcagggt aatgtcgcca ttaaaactggc gcaggcagcc aaagagttgc tccgcttcta 60
 cccagtcggc agcgacaact tgcgttaaag tcgcaaaatt atcatctgca ctactgcgt 120
 gacgtaagcg gatggagtgg ccggaaacct catagtacc gccaccagt tggcctgcat 180
 cgctttgtag cgtacgcgcg gcattggcaa taagattcag atactcagac tcttccgggg 240
 ctttcgccag cataaaagag gaggatgctc gcgtatgcag caactgctcc agcgcaaatt 300
 gcagccgchg ttgagtatca ctgaataaag gatcgttttc gtcaatcaaa tgtggctgag 360
 caaatatttc ctgatagcta tcggtatcag gaaccaggctc acgccatgca agtttcgtaa 420
 tggtcaaaagt tgatgttttt tagtctgttg tcaaagccgc nattataccn gtaaccggca 480
 ctacagcaca cgtagaaagc acccgacaat actcctggca tgggcgttaa agctcacagg 540
 atggagatct tttcttcaact ggctaaaaa gctgatattc tgtaaagagt tacacngtaa 600
 cattgagatc gctatgaaat atcaacaact tggaaaatct tgnaaagcng gttggaaaat 660
 ggaaagtatc tggttaagaa gc 682

<210> 408
 <211> 309
 <212> DNA
 <213> Escherichia coli

<400> 408
 ggggatccgg cagaatTTTta cgctgaccaa tgacgcgacg acgtggcatg gaaatactcc 60
 gttgttaatt caggattgtc caaaactcta cgagtttagt ttgacattta agttaaAACg 120
 tttggcctta cttaacggag aaccattaag ccttaggacg cttcacgcca tacttggaac 180
 gagcctgctt acggtctTTta acgccggagc agtcaagcgc accacgtacg gtgtggtaac 240
 gaacacccgg gaggtctTTta acacgaccgc cacggatcag gatcacggag tgctcctgca 300
 gccaaagctt 309

<210> 409
 <211> 1167
 <212> DNA
 <213> Escherichia coli

<400> 409
 gtcgacccat ctgtccattg agcggacagt ttgtgcaaca ctatttttgtt gaccggaaaa 60
 tggaacactt tccgcaatgc ctgttgctat cacgcttaaa ccatttcatt gcgatttaca 120
 cagaacggac gtcctgtcgc agtatattaa gtcgtcgata gaaacaagca ttgaaaggca 180
 cagcagtagt caaacagtgt gaaacgctac tggcgcctta cagcgcaaaa aggctgggtga 240
 ctaaaaagtc accagccatc agcctgattt ctcaggctgc aaccggaagg gttggcttat 300
 ttaacttcaa cttcagcgcc agcttcttcc agagcttttt tcagtgtctc tgcgtcgtct 360
 ttgctcacgc cttctttcag agcagccggg gcagattcta ccaggctctt agcttctttc 420
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 gctttcagaa ttacgtcgaa ttcagttttt tcttcagcag cttcaaccgg gccagcagct 540
 acagctacag cagcagcagc ggaaacaccg aatttttctt ycattgcaga gatcaagttc 600
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 catttaaatk gttcctgaat atcagaataa gtttatacgt aagcgaatgc gttaaaaaga 720
 taactgcgaw taagcagctt ytttcgcatc gcgtacagma gccagagtac gaaccagttt 780
 gccagccgaa gcttctttca tggttgccat caggcgtgca attgcttctt cgtaggctcg 840
 cagagttgcc aggcggtcga tctgagacgc cgggatcagc tcaccttcaa aggcagcggc 900
 tttgacctca aattttgcat tcgctttcgc gaactctttg aacagacgag cagcagcgcc 960
 cgggtgttcc atagagtatg caatcagggt cggaccaaca aacgcgtctt tcaggcactc 1020
 gaacggagta ctttcaacag cacggcgag caggggtgta cgaacaacac gcatgtatac 1080
 gccagcttcg cgacctgctt tacgcagttc agtcatttta tctacagtta cgcccacggg 1140
 aatccgcaac tactgcaagc caagctt 1167

<210> 410
 <211> 404
 <212> DNA
 <213> Escherichia coli

<400> 410
 caacmctatt ttgktggacc ggaaaakgga acacttttccg cawkgcctgt tgctatcacg 60
 cttaaaccat ttcattgcga tttacacaga acggacgtcc tgtcgcagta tattaagtcg 120
 tcgatagaaa caagcattga aaggcacagc agtagtcaaa cagtgtgaaa cgctactggc 180
 gccttacagc gcaaaaaggc tgggtgactaa aaagtcacca gccatcagcc tgatttctca 240
 ggctgcaacc ggaagggttg gcttatttaa cttcaacttc agcgccagct tcttccagag 300
 cttttttcag tgcttctgcg tcgtctttgc tcacgccttc tttcagagca gccggtgcag 360
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcg 404

<210> 411
 <211> 152
 <212> DNA
 <213> Escherichia coli

<400> 411
 agagcttttt tcagtgtctc tgcgtcgtct ttgctcacgc cttctttcaa gagcagcccc 60
 gtgcagattc taccaggtct ttagcttctt tcagaccag gccagttgcg ccacgtactg 120
 ctttgataac agcaactttg ttagcgccag ca 152

<210> 412
 <211> 825
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(825)
 <223> n = A,T,C or G

<400> 412
 gatccgctga cccatctgtc cattgagcgg acagtttgtg caacactatt ttgttgaccg 60
 gaaaatggaa cactttccgc aatgcctggt gctatcacgc ttaamccatt tcattgcat 120
 ttacacagaa cggacgtcct gtcgcagtat attaatgctg cgatagaaac aagcattgaa 180
 aggacagca gtagtcaaac agtgtgaaac gctactggcg ccttacagcg caaaaaggct 240
 ggtgactaaa aagtcaccag ccatcagcct gattttctcag gctgcaaccg gaaggggttg 300
 cttatttaac ttcaacttca gcgccagctt cttccagagc ttttttcagt gcttctgctg 360
 cgtctttgct cagccttctt ttccagagcag ccgggtgcag attctaccag gtcttttagct 420
 tctttcagac ccaggccagt tgcgccacgt actgctttga taacagcaac tttgttagcg 480
 ccagcagctt tcagaattac gtcgaattca agtttttctt tcagcagctt caaccgggcc 540
 agcagctaca gctacagcag cagcagcggg aacaccgaat ttttcttyca ttggcagaga 600
 tcaagttcta caacgtccat tacagacata gctgcaactg cttcaatgat tkgatcttwa 660
 gtgatagaca tttaaattgt tcctgaatat cagaataagt ttatacgtaa gcgaatgcgt 720
 taaaaagata actgcgatta agcagcttct ttcgcatcgc gtacagcagc cagaggtcga 780
 accagtttgc cagccgaagg ttggcttttc agcctnnnch natta 825

<210> 413
 <211> 425
 <212> DNA
 <213> Escherichia coli

<400> 413
 agtagtcaaa caggtgkgra acgctactgg cgccttacag cgcaaaaagg ctggtgacta 60
 aaaagtcacc agccatcarc ctgatttctc aggctgcaac ccggaagggt tggcttattt 120
 aacttcaact tcagcgccag cttcttccag agcttttttc agtgcttctg cgtcgtcttt 180
 gtcacgcct tctttcagag cagccgggtgc agattctacc aggtcttttag cttctttcag 240
 acccaggcca gttgcgccac gtactgcttt gataacagca actttgtag cgccagcagc 300
 tttcagaatt acgtcgaatt cagttttttc ttcagcagct tcaaccgggc cagcagctac 360
 agctacagca gcagcagcgg aaacacccga atttttcttc cattgcagag atcaagttct 420
 acaac 425

<210> 414
 <211> 126
 <212> DNA
 <213> Escherichia coli

<400> 414
 agagcttttt tcagtgtctt tgcgtcgtct ttgctcacgc cttctttcag agcagccggt 60
 gcagattcta ccagggtcttt agcttctttc agaccaggc cagttgcgcc acgtactgct 120
 ttrata 126

<210> 415
 <211> 264
 <212> DNA
 <213> Escherichia coli

<400> 415
 ctgcmacccg garggggttg cttatttaac ttcaacttca gcgccagctt cttycagagc 60
 ttttttcaag tgcttctgct tgcgtctttg tcacgccttc tttcagagca gccggtgcag 120
 attctaccag gtcttttagct tctttcagac ccaggccagt tgcgccacgt actgctttga 180
 taacagcaac tttgttagcg ccagcagctt tcagaattac gtcgaattca gttttttctt 240
 cagcagcttc aaccgggcca gcag 264

<210> 416
 <211> 201
 <212> DNA
 <213> Escherichia coli

<400> 416
 cgcataccct gcagcatcgg cccgatggag atcaggctcg cagaacgctg taccgctttg 60
 taggtggtgt taccggtgtt cagatccggg aagatgaaca cggtagcgcg acctgcaacc 120
 ggagagttcg gcgctttgga tttcgcaacg tcagccatta ccgcagcgtc gtactgcagc 180
 ggaccgtcga tcatcaggtc a 201

<210> 417
 <211> 239
 <212> DNA
 <213> Escherichia coli

<400> 417
 aattcagcag ttgacagtgg cataaacgta actggtgact tttgcccggc atgacgccgg 60
 gcttttttta ttattccgtg acttccagcg tagtgaaggc aaactttctcg ccatcaaata 120
 gcccttgact ggtagtttt agcgcgggga tcaactggcag agaaagaaac gccatctgaa 180
 taaacggctc atcgggtaac ggaccgcatt cacgggcggc ggctttcaag gcgtcaatt 239

<210> 418
 <211> 223
 <212> DNA
 <213> Escherichia coli

<400> 418
 ttcttttttt cgtcaacggt gtccagaatc atttttattta cctcgggtac ttatgctgat 60
 ttttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa 120
 ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
 aatactatth aaatattatt ttgagcatat gcacataagg ttg 223

<210> 419
 <211> 223
 <212> DNA
 <213> Escherichia coli

<400> 419
 ttcttttttt cgtcaacggt gtccagaatc atttttattta cctcgggtac ttatgctgat 60
 ttttattatt atggggaagg tgttatttat gagtttcatt tatgccgtaa cgacaatgaa 120
 ctcgggaatt agtataagca gcgcgagaat aataatcatt gtgcaaatgc taatttaatt 180
 aatactatth aaatattatt ttgagcatat gcacataagg ttg 223

<210> 420
 <211> 212
 <212> DNA
 <213> Escherichia coli

<400> 420
 aatagcgggt atgcacgcct ttcttttttt cgtcaacggt gtccagaatc atttttattta 60
 cctcgggtac ttatgctgat ttttattatt atggggaagg tgttatttat gagtttcatt 120
 tatgccgtaa cgmcaatgaa ctcgggaatt agtataagca gcgcgagaat aataatcatt 180
 gtgcaaatgc taatttaatt aatactatth aa 212

<210> 421

<211> 438
 <212> DNA
 <213> Escherichia coli

<400> 421
 ccctgtaaat tatcgcccgt ggcataaaaa ctgctgccaa acgcccgtctt tgccagcagc 60
 caggccataa atgccaccag aattatcgtc aaccaaccaa ttgctgaaac gccaaagcagc 120
 agcggggcgg agagctgttt cagttcggcg ggtaaccctt caatccattt gccgccagtc 180
 cacagcaaca tgatgcctct gtacaaccct aacgtgccaa ggggtggcaac aatggcaggg 240
 atcttttagcc acgcgaccag gacaccgttg aaaaatcccg cgagcaaacc aagcagtaaa 300
 gtcgcgacac aagcaacagg tagtgaatat cctgcgttca gtaacatccc caacagcacc 360
 gcgcacattc cgggtaatcg aaccccactt gaaacatcaa tattgsgsgt aagcattwcc 420
 aagcgttcgs gcccakg 438

<210> 422
 <211> 682
 <212> DNA
 <213> Escherichia coli

<400> 422
 aattcccggg gatccgtcga ccgtgcgctt ccggttggtg caacccgcga aatggcgcg 60
 cggtaaagtat ggcgggggta ttccctcccc gttgaggaca ccggttggtc aggttgacca 120
 tacgcttaag tgacaacccc gctgcaacgc cctctgttat caattttctg gtgacgtttg 180
 gcggtatcag ttttactccg tgactgctct gccgcccttt ttaaagtga ttttgtgatg 240
 ttgtgaatgc ggctgagcgc acgcggaaca gttaaaacca aaaacagtgt tatgggtgga 300
 ttctctgtat ccggcggtta ttgttaactg gttaacgtca cctggaggca ccaggcactg 360
 catcacaaaa ttcatgtgtg aggacgcgat aatgaaaacg ttattaccaa acgttaatac 420
 gtctgaaggt tgttttgaaa ttggtgtcac tatcagtaac ccagtattta ctgaagatgc 480
 cattaacaag agaaaaacaag aacgggagct attaaataaa atatgcattg tttcaatgct 540
 ggctcgttta cgtctgatgc caaaaggatg tgcacaaatga attcagcatt tgtgcttgtt 600
 ctgacagttt ttcttggttc cggagagcca gttgatattg cagtcagtgt tcacaggaca 660
 atgcaggagt gatgactgca gc 682

<210> 423
 <211> 600
 <212> DNA
 <213> Escherichia coli

<400> 423
 ggggatccga ttgtgactgc tctgccgccc tttttaaagt gaattttgtg atgtggtgaa 60
 tgcggctgag cgcacgcgga acagttaaaa caaaaacag tggtatgggt ggattctctg 120
 tatccggcgt taattgttaa ctggttaacg tcacctggag gcaccaggca ctgcatcaca 180
 aaattcattg ttgaggacgc gataatgaaa acgttattac caaacgttaa tacgtctgaa 240
 gggtgttttg aaattgggtg cactatcagt aacccagtat ttactgaaga tgccattaac 300
 aagagaaaaac aagaacggga gctattaaat aaaatatgca ttgtttcaat gctggctcgt 360
 ttacgtctga tgccaaaagg atgtgcacaa tgaattcagc atttgtgctt gttctgacag 420
 tttttcttgt ttccggagag ccagttgata ttgcagtcag tgttcacagg acaatgcagg 480
 agtgtatgac tgcagcaacc gaacagaaaa ttcccgttaa ctgttaccgg gtcgataaag 540
 ttattcacca ggataatatc gaaatcccgg caggtcttta aacagttccg taataaataa 600

<210> 424
 <211> 100
 <212> DNA
 <213> Escherichia coli

<400> 424
 gggatccagc aagaagatgc ggttgtagcg tcatcacgca gatgcgcaaa gctactcagc 60

aactgacctt tcttcgcaat aagcacgcca ttagcgtcac 100

<210> 425
<211> 465
<212> DNA
<213> Escherichia coli

<400> 425
tcgcgtgttt accttcaaca tcggtaactt tctggcggat agtttcacgg taagcaacct 60
gcggtttacc tacgttcgct tcaacgttga attcacgctt catacggcca acgatgatgt 120
cgagggtcag ttcgcccata cccgcgatga tgggtctggt agattcttcg tcagtcata 180
cacggaaaga cgggtcttct ttagccagac ggcccagagc cagacccatt ttttcctggt 240
cagctttggt tttcggttca actgcgatgg agattaccgg ctcagggaaat tccatacgtt 300
ccagaatgat cggcgcaccc gggtcacaca gggtgtcacc agtgggttacg tctttcagac 360
cgatagcagc agcgatgtcg cccgcgcgaa cttctttgat ctcttcacgt ttggttagcgt 420
gcatctgaac gatagaccg aaacgctcac gtgcagcttt cacgg 465

<210> 426
<211> 653
<212> DNA
<213> Escherichia coli

<220>
<221> misc_feature
<222> (1)...(653)
<223> n = A,T,C or G

<400> 426
tgatcggctc aagcagaact ggtttcgttt tcttaaagcc ttcttttaaag gcgatagaag 60
cagccagttt aaacgccagt tcagaggagt caacgtcatg gtaagaaccg aagtgcagac 120
gaatacccat gtctactacc gggtagcctg ccagcggacc tgctttcagc tgttcctgga 180
tacctttatc aacggccggg atgtattcgc cagggattac accaccttta atgtcgttga 240
tgaactcgta gcctttcggg tttgaacccg gctccagcgg gtacatgtcg ataacaacat 300
gaccatactg accacgacca ccagactggt tcgcgtgttt accttcaaca tcggtaactt 360
tctggcggat agtttcacgg taagcaacct gcggtttacc tacgttcgct tcaacgttga 420
attcacgctt catacggcca acgatgatgt cgagggtcag ttcgccatac cccgcgatgat 480
ggctgggtag attcttcgtc agtccataca cggnaagacg ggtcttnttt agccagacgg 540
gccagagnca gacccatttt tttctggcag ctttggnntc ggtcaactgc gatggaaata 600
cccggctcaa ggaattcata cgtttcanaa tgatcggggc attccgggtc aca 653

<210> 427
<211> 268
<212> DNA
<213> Escherichia coli

<400> 427
ctttcttaaa gccttcttta aaggcgatag aagcagccag tttaaagccc agttcagagg 60
agtcaacgtc atggtaagaa ccgaagtgcg gacgaatacc catgtctact accgggtagc 120
ctgccagcgg acctgctttc agctgttcct ggataccttt atcaacggcc gggatgtatt 180
cgccagggat tacaccacct ttaatgtcgt tgatgaactc gtagcctttc gggtttgaac 240
ccggtccag cgggtacatg tcgataac 268

<210> 428
<211> 330
<212> DNA
<213> Escherichia coli

<400> 428
 gttttgggga gatgtaagg ctaatctgaa tggctgcatt ccttgtttaa ggaaaaacga 60
 atgactgatt gccgatacct gattaaacgg gtcatacaaaa tcatcattgc tgttttacag 120
 ctgacccctt tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
 cggacgcacc ttttaataact ataaataagt gtctgggcag atactatata aattaactta 240
 gtgaatgatt atgctaattgt catcaattaa ataaatataa tggcgtaag gcttcccagt 300
 aatataatta atactctact tccagagtag 330

<210> 429
 <211> 465
 <212> DNA
 <213> Escherichia coli

<400> 429
 gttttgggga gatgtaagg ctaatctgaa tggctgcatt ccttgtttaa ggaaaaacga 60
 atgactgatt gccgatacct gattaaacgg gtcatacaaaa tcatcattgc tgttttacag 120
 ctgacccctt tgttcttata acacaaggaa acgtacttaa ggtgcgtccg gtgaaccagt 180
 cggacgcacc ttttaataact ataaataagt gtctgggcag atactatata aattaactta 240
 gtgaatgatt atgctaattgt catcaattaa ataaatataa tggcgtaag gcttcccagt 300
 aatataatta atactctact tccagagtag aatattaaat tttatccgcg tgggtgcatca 360
 gcacaaattt atcccacaac tgttcttctg tctcgacatg cgccgatct ttcacaatag 420
 tattggggat cgggcacacc ttctggcagg ttggtgtctc gtagt 465

<210> 430
 <211> 379
 <212> DNA
 <213> Escherichia coli

<400> 430
 aatctgaatg gctgcattcc ttgtttaagg aaaaacgaat gactgattgc cgatacctga 60
 ttaaacgggt catcaaaatc atcattgctg ttttacagct gatccttctg ttcttataac 120
 acaaggaaac gtacttaagg tgcgtccggt gaaccagtcg gacgcacctt taataactat 180
 aaataagtgt ctgggcagat actatataaa ttaacttagt gaatgattat gctaattgtca 240
 tcaattaaat aaatataatg gcgttaaggc ttcccagtaa tataattaat actctacttc 300
 cagagtagaa tattaaattt tatccgcgtg gtgcatcagc acaaatttat cccacaactg 360
 ttcttctgtc tcgacatgc 379

<210> 431
 <211> 443
 <212> DNA
 <213> Escherichia coli

<400> 431
 aagatgatgt gatgagaaa tcaatttgaa taagacaata ttaagagcta aaaaaatgtc 60
 aaaaaacact aaatcaaaaa ataattggcat tagaaaaatat aatgcgaaaa cggaggtgaa 120
 attagtttat ttcaaatgag gaaaatctcc cggcgaaaaa accgggagat gaaagtgtga 180
 tgggtatcaa ataaacaaca gaggagaaat ttttaacgca gccattcagg caaatcgttt 240
 aatcccattg cctggcggat aagttgcggc ttaacgccag gaagcgtgtc ggccagtttc 300
 aaaccaatat cacgcagcag ttttttcgcc ggattggtac cggaacacag atcgcggaat 360
 ccctgcatac cagccagcat caacgccgca ctgtgcttgc ggctacgctc atagcgacgc 420
 agataaatgt actgcccgat gtc 443

<210> 432
 <211> 638
 <212> DNA
 <213> Escherichia coli

<400> 432
caggggggttt gttgtgǵgca atgatgcatt taagttatcg tctgcagata gaggagatat 60
tacaataaac aacgaatcag ggcatttgat agtcaatacc gcaattctat caggagatat 120
agtcactcta agaggaggag aaattagggtt ggtattatag cttgtgcgcg ccatgattgg 180
cgcgcaattt aaacttagtg ctttacatcg ctattgtctt gatttctttg aattatttta 240
taaattaaaa aaacgactgt tatgtataag caaagggtccg aacgaaaaat acattccaaa 300
taaatgcttg cttaaactct tatatccttc cccgaaaaat gacacataaa attgagatat 360
tccaaaaaga gatactacaa ataaagatgc ctttatttta ttatttctaa taaaaataga 420
agcaataaaa aataataaca atgatataaa tctaattgtt tttaatatat tgtcttttat 480
gttagtaata gtcgttagta tgtttgattc tccatatatt acgtgtagtt ttttatatac 540
atggaaataa ttttctttat actgagacat cacaccatca tcaaattggaa gtttgaagat 600
ggtgcttggt ttgctaacca ataaaaagag tgcattcg 638

<210> 433

<211> 299

<212> DNA

<213> Escherichia coli

<400> 433
ctttacctgg catgatccac ttcgccagaa taccggcaat aagcccaaaa ataatccatg 60
acagaatgcc cattgtttcc tcacttatct gttttgcatt agcgggtag tcgctgataa 120
aaagcatagc acaacatcgg gagggcaaga tttgtgacga gcatacagga ggtttttttg 180
cgatggcgca gaaattgcgc catcaacgat cagtgataat taccaaccac aaacatcatg 240
ttcgttttcc gtgtcataag aacgtacggt attcaccaga tcttttatca cttcagccg 299

<210> 434

<211> 388

<212> DNA

<213> Escherichia coli

<400> 434
gaaaaaggag gcaatatcgg gtaaaggcat tagcccgacg aatacgtcgg gctacaaata 60
ttattgtgct gcagggtgtt tagcgggttg ttgatccaca ggttctaact ggaagaccac 120
atcgacctga tcatcaaact gaatagcggc ctgctcgtaa gtttcctggg cggacaccgg 180
cgcggcacg gctttcatca tccgcacat tgggctgggc tgatagtgg aaacatggta 240
gcgcacgcta tataccggcc ccagtttacg atgaaagccg ttcgccagtt cctgcgcctg 300
atgaatcgcg ttatcaatcg ctgccttacg cgctttgtct ttataggcat ccggctgcgc 360
cacgccagc gacacagaac gaattccc 388

<210> 435

<211> 351

<212> DNA

<213> Escherichia coli

<400> 435
ctatccttga tgaaaccgcg agcaaagata ggtgattacg tcatggtttt acagaaaatt 60
acagaaaaag gaggcaatat cgggtaaagg cattagcccg acgaatacgt cgggctacaa 120
atattattgt gctgcagggt ttttagcggg ttgttgatcc acaggttcta actggaagac 180
cacatcgacc tgatcatcaa actgaatagc ggctgctcg taagtttcct gggcggacac 240
cggcgcgga tcggctttca tcatccgcac cattgggctg ggctgatagt tggaacatg 300
gtagcgcacg ctatataccg gccccagttt acgatgaaag ccgttcgcca g 351

<210> 436

<211> 762

<212> DNA

<213> Escherichia coli


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<220>
<221> misc_feature
<222> (1)...(762)
<223> n = A,T,C or G

<400> 436
aattatgaaa cactgtcttg aatcgtctga atgacgggca catttgcgag cacgcatcca      60
gtaataacac aggaaactat tttatctacg cgttagcgat agactgcttg catggcgaaa      120
ggaggtaagc cgacgatttc agcgggacgc tgaaacggga aagcccctcc cgaggaaggg      180
gccataaata aggaaagggg catgatgaag ctactcatca tcgtgggtgct cttagtcata      240
agcttccccg cttactaaga ctaccagggc gggggaaacc ccgctctacc ctcaactctg      300
aaagtatgcc ttcacgataa gattgtcaat ccgcaggcct tgtagtctgc gatcctgcca      360
gcaaatattc tttgcgagtc gttacgcaat aatcacagag gaaactatct tattcacgcg      420
ttagcgatag actgcattca gggcgaaagg aggtaagccg atgatttcag cgggacgctg      480
aaacgggaaa gcctctcccc gagaagaggg cttttaataa ggaaagggtt atgatgaagc      540
acgtcatcat actggtgata ctcttagtga ttagcttcca ggcttactaa gaacaccagg      600
gggaggggga aacctcttcc taaccctcac ttctgaaatt ggggtgctatg acgctggcgt      660
tactgcttan cgctaccagt ttgtctgccc tggcggttgt aacgccagat cggtacccgt      720
ttggatattt taatgaaagc cgacaaatca atcancgtga cg                                762

<210> 437
<211> 292
<212> DNA
<213> Escherichia coli

<400> 437
cacatttgcg agcacgcatt cagtaataac acaggaaact attttatcta cgcgttagcg      60
atagactgct tgcattggcg aaggaggtaa gccgacgatt tcagcgggac gctgaaacgg      120
gaaagcccct cccgaggaag gggccataaa taaggaaagg gtcatgatga agctactcat      180
catcgtgggtg ctcttagtca taagcttccc cgcttactaa gactaccagg gcgggggaaa      240
ccccgctcta cctcactccc tgaaagtatg ccttcacgat aagattgtca at                                292

<210> 438
<211> 631
<212> DNA
<213> Escherichia coli

<400> 438
atttacactt tttacgaaat catgggatca ctaacaaaat atcgcttgct agttatattg      60
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca      120
ttaaaaataa gatgttgctg ggtgcgcttt tgctgggttac cagtgccgcc tgggccgcac      180
cagccaccgc gggttcgacc aatacctcgg gaatttctaa gtatgagtta agtagtttca      240
ttgctgactt taagcatttc aaaccagggg acaccgtacc agaaatgtac cgtaccgatg      300
agtacaacat taagcagtgg cagttgcgta acctgcccgc gcctgatgcc gggacgcact      360
ggacctatat gggtagcgcg tacgtgttga tcagcgacac cgacggtaaa atcattaaag      420
cctacgacgg tgagattttt tatcatcgct aaaaaaagcc cctcatcat gagggggaaa      480
tgcagacacc ttgttatttt ttattattag ccacttgctc gtcttgcttg ttattagtcg      540
tatttcacgt tgattaatgc ggttgccctc agtgcgccag atttaacttt gtttgtatcg      600
tagacgtagt aactggctgt tatcggaatt g                                631

<210> 439
<211> 566
<212> DNA
<213> Escherichia coli

<400> 439
tatggcagga aagatatgcg actgatatta cagatcccca aagtggagag tttatgacca      60

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ttaaaaataa	gatgttgctg	ggtgcgcttt	tgctggttac	cagtgccgcc	tgggcccgcac	120
cagccaccgc	gggttcgacc	aatacctcgg	gaattttctaa	gtatgagtta	agtagtttca	180
ttgctgactt	taagcatttc	aaaccagggg	acaccgtacc	agaaatgtac	cgtaccgatg	240
agtacaacat	taagcagtgg	cagttgcgta	acctgcccgc	gcctgatgcc	gggacgcact	300
ggacctatat	gggtggcgcg	tacgtgttga	tcagcgacac	cgacggtaaa	atcattaaag	360
cctacgacgg	tgagattttt	tatcatcgct	aaaaaaagcc	ccctcatcat	gagggggaaa	420
tgacagaccc	ttgttatttt	ttattattag	ccacttgctc	gtcttgcttg	ttattagtcg	480
tatttcacgt	tgattaatgc	ggttgccctc	agtgcgccag	atttaacttt	gtttgtatcg	540
tagacgtagt	aactggctgt	atcgaa				566

<210> 440

<211> 339

<212> DNA

<213> Escherichia coli

<400> 440

cgtattcaca	tccttttgat	tggtgataac	atgcgaatcg	gtattatttt	tccggttgta	60
atcttcatta	cagcggtcgt	atcttttagca	tggtttttta	ttggcggcta	tgctgccccg	120
ggagcataaa	gatgaaaaaa	acaacgatta	ttatgatggg	tgtggcgatt	attgtcgtac	180
tcggcactga	gctgggatgg	tggtaacgtc	acctctaaaa	aatagcaaag	gctgcctgtg	240
tgacgccttt	gtgcaattta	agcgtaaact	tttaatcttc	ctgtagataa	atagcacgac	300
aatcgcacca	ataacggcaa	ccacgaagct	gccaaaatt			339

<210> 441

<211> 376

<212> DNA

<213> Escherichia coli

<400> 441

catgaatatt	taaaaaggaa	aacgacatga	aaccgaagca	cagaatcaac	attctccaat	60
cataaaatat	ttccgtggag	cattttatta	ttgaatatag	aggtttaact	ccggtaaaaa	120
acaaagaagc	attgaatgca	gggaaaaata	atatggccat	aaaaaacatc	gaaagaaact	180
cttttaattt	aacatgtaaa	cgcattggtta	atcctcatat	cacgggtgga	gtgttaagaa	240
catacataaa	tgagagtcag	ttttcccttt	tccatttatc	aagttcctgt	tgccgtttta	300
gtccatctct	aattgcatat	tttaattttt	ctgataaatg	gcattgagca	tcgatttcat	360
ttaaaacaac	tgtaca					376

<210> 442

<211> 446

<212> DNA

<213> Escherichia coli

<400> 442

ttacgatagc	tattagtaaa	aatataagag	ttagctgtat	tgttatgtct	gtggcgaaat	60
tgactacctt	cgtttttttg	attaagaatg	atctttattat	cgtaagttaa	attacatgaa	120
tatttaaaaa	ggaaaacgac	atgaaaccga	agcacagaat	caacattctc	caatcataaa	180
atatttccgt	ggagcatttt	attattgaat	atagagggtt	aactccggta	aaaaacaaag	240
aagcattgaa	tcaggggaaa	aataatatgg	ccataaaaaa	catcgaaaga	aactctttta	300
atttaacatg	taaacgcag	gttaatcctc	atatcacggg	tggagtgtta	agaacataca	360
taaatggagt	catgttttcc	cttttccatt	tatcaagttc	ctggttgccgt	tttagtccat	420
ctctaattgc	atattttta	at	ttttct			446

<210> 443

<211> 388

<212> DNA

<213> Escherichia coli

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<220>
<221> misc_feature
<222> (1)...(388)
<223> n = A,T,C or G

<400> 443
tcaccccggt gccgattttc aggcatacctg atttaactta gcacccgcaa ctttaactaca      60
ggaaaacaaa gagataaatg tctaatacctg atgcaaatac agccgatttt ttaatacttta      120
cggactttta cccgcctggt ttattaattg cactgtnatc cgggcgttcg cccgctttta      180
tcacaatagg ctgtgtagcc tgggcctggt tctctttcac ccgcgccaga gcggcagcaa      240
tcgcatcttt atctttggct gcaggttgaa cggctgcgct cttatgtcgt tcaaggcgag      300
ccgctttttc gcgctccaga cgagcctggc gcgcttcgaa acgcgctttg gcttctgcgg      360
cncgcttttc ttctgacga atagccgc
cncgcttttc ttctgacga atagccgc      388

<210> 444
<211> 209
<212> DNA
<213> Escherichia coli

<400> 444
aattttaata acgctatctg cggataaagc agaatagggt gttaacccca gacataaacc      60
gaggaaaata atgttattgt atttcataat ctattgttcc ttagcgacag attgctgtct      120
gctggttcag taaggtagca ggagaaactt caggaagctt gtactcgaca atacagtttg      180
agtttttatc ttgccccat gaaacctgt
agtttttatc ttgccccat gaaacctgt      209

<210> 445
<211> 341
<212> DNA
<213> Escherichia coli

<400> 445
catcctcaat accgttaaata gcaacccgaa cccccgttgt ccccttgctg cattcaactta      60
acgtaatctg aaaagggacg gctggacttg tgctaccggt cgttggaat tgtctggcac      120
tggttttttg gagatctacg gtaaaattaa gcgaatccga tgagactgtg cagccataat      180
cgaggacgcg cccgctaatt ttaataacgc tatctgcgga taaagcagaa taggtgggta      240
accccagaca taaaccgagg aaaataatgt tattgtattt cataatctat tgttccttag      300
cgacagattg ctgtctgctg gttcagtaag gtaccaggag a
cgacagattg ctgtctgctg gttcagtaag gtaccaggag a      341

<210> 446
<211> 697
<212> DNA
<213> Escherichia coli

<400> 446
agatttactg ccaattttccg gcagatcgga aagggttaam ccatattgat ccataagggt      60
acgaatcmcg ggctataaccg ccaggcatgg cttgagccat ggcatataat tccgcaaatt      120
cgggcgctga ttcttcccac gcggttattt tggcacacac cagatccagc aagggggttt      180
caggatcggt gagcagcaga tgatctacca gttccagcgc ctgggtgtat tgttcctcgt      240
tctgaatacc cgccagaaaa ggtgccacag cagttagctt ttctcctgct tgcaagatgt      300
cggcaatcgc aatcattttt tccccttagt acgatgaaca gcggtaaaaga aatcgtattc      360
tttatgcgtc ataacttcac gtatgtagca cttttgcgat tcaaaaaaga ccattgctac      420
aacacgtaat tcattgcccc caacattgaa aacataatgc ttatccagat atttgaagtt      480
atccagagat gggaataactg cttttaatga ctacaggtttt ttgaaatatc ccttagcaat      540
cgtgktcccc agagccacca actccgtttt atgttgcggg tatttttccg cagcatcttt      600
caatgctttt tgagttatca ggtgcattct tcatcacgtc cgtkgmcaaa ttggcaatat      660
gataacatcc gttgccagat tggcacggat gaattat
gataacatcc gttgccagat tggcacggat gaattat      697

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<210> 447
 <211> 215
 <212> DNA
 <213> Escherichia coli

<400> 447
 aattaataac ttttcgttag gcagttttgg gtgtgagttg caagagggga gactactgaa 60
 taactcaagt ttataatcg aggggaaaat ggtgatggcg ttcatagcaa aacgccctca 120
 accataaagg tcgagggcgc ttaagatggt aaaaacccgc tatccgttaa aaaacaatgt 180
 tcaactaagg tcagtgcacat tgcgctaaaa aagcg 215

<210> 448
 <211> 395
 <212> DNA
 <213> Escherichia coli

<400> 448
 gcattattca tgagaaatgt gtatcgtaaa tcaactgaaa ttaacgcaac catttgttat 60
 ttaaggttta attatctgtg tgtgatattt tattgaatgt tttaaatatt gtttttattg 120
 gcattgctat aatattggtt atcatttgct gaatggattc agtcttaatg agtgggtttt 180
 taagggacag gcatagagta atgatacgta tgcataacca acatctttac tcattatgtc 240
 attgaatggt gacgctatgt gtttatgagg gagaggattt ttcagttgat ctggattggt 300
 aaattcatat aatgcgcctt tgctcatgaa tggatgccag tatgtagtgg gaaattataa 360
 atattgaaat agtccaacta cttctttatt accaa 395

<210> 449
 <211> 641
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(641)
 <223> n = A,T,C or G

<400> 449
 ataatcaggt aagaaaaggt gcgcggagat taccgtgtgt tgcgatatat tttttagttt 60
 cgcgtagcaa tacatcagtg gcaataaaac gacatatcca gaaaaatata cactaagtga 120
 atgatatctt ccgatttatc ttaatcgttt atggataacg gcaaagggct tcgttttttc 180
 ctatacttat tcagcactca caaataaaag aacgccaatg aaaattatac tctgggctgt 240
 attgattatt ttcttgattg ggctactggt ggtgactggc gtattttaaga tgatatttta 300
 aaattaatta atgtcatcag gtccgaaaat aacgagaata tttcagtcctc tcacctctgt 360
 gcgctcctgt catgtgcatt gcttcatata atcactggcg caaggagcgc cgcaggcgna 420
 gnntgcncgn cgnccacct naccccatgc cgaacttcag aantgaaaac nccntaacnc 480
 cgatngtcgg cggngcctc cccatgcnan agtangggaa ntgccangcg ncnntataaa 540
 cgaaaggctn attncaaaga ctgggccttn cntttatctg atgtttgtcg gagaacgctc 600
 tcctgagnan gacaaatncc gccgggagcg gatttgaacn t 641

<210> 450
 <211> 314
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(314)
 <223> n = A,T,C or G

<400> 450
gaactacgag taagaatagc tncgaattcc cgtttatgga taacggcaaa gggcttcggt 60
ttttcctata cttattcagc actcaciaat aaaggaacgc caatgaaaat tatactctgg 120
gctgtattga ttattttcct gattgggcta ctgggtggtga ctggcggtatt taagatgata 180
ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatatttca gtctctcatc 240
ctgttgcgct cctgtcatgt gcattgcttc atataatcac tggcgcaagg agcgcgagcagg 300
gggntntnnt cttt 314

<210> 451
<211> 236
<212> DNA
<213> Escherichia coli

<400> 451
atatacacta agtgaatgat atcttccgat ttatcttaat cgtttatgga taacggcaaa 60
gggcttcggt ttttcctata cttattcagc actcaciaat aaaggaacgc caatgaaaat 120
tatactctgg gctgtattga ttattttcct gattgggcta ctgggtggtga ctggcggtatt 180
taagatgata ttttaaaatt aattaatgtc atcaggtccg aaaataacga gaatat 236

<210> 452
<211> 418
<212> DNA
<213> Escherichia coli

<400> 452
cggagattac cgtgtgttgc gatataatctt ttagtttcgc gtggcaatac atcagtggca 60
ataaaacgac atatccagaa aaatatacac taagtgaatg atatcttccg atttatctta 120
atcgtttatg gataacggca aagggtctcg ttttttccta tacttattca gcactcacia 180
ataaaggaac gccaatgaaa attatactct gggctgtatt gattattttc ctgattgggc 240
tactggtggt gactggcgta tttaagatga ttttttaaaa ttaattaatg tcatcaggtc 300
cgaaaataac gagaatattt cagtctctca tctgtttgcg ctctgtcat gtgcattgct 360
tcatataatc actggcgcaa ggagcgcgca gggggcggcc aatcgccgcc gccccctg 418

<210> 453
<211> 551
<212> DNA
<213> Escherichia coli

<400> 453
aacaatttgc ccatgcgctc ggtcatgcgc tgcacgccc ggccattttg sgcgtccccg 60
cgaccgccat tgcactgtta atgggcgaat cttcagtact ggtattaggt ggacaacgcg 120
cgctgcctaa acggctggaa gaagcggggt ttgcgtttcg ctggtacgat ttagaagagg 180
cgctggcgga tgcgttcgc tgatgtggtt tacagcaaac atccgccagt taactccccg 240
tgttacagga ttagtggctt tgcgcgataa gatcgtctgg tgaaagtcgg gtcaccatca 300
taactaactc tctgtctaaa cctctatcca gcactctctg agcaatacgc agggcttctt 360
cgtgtttgcc ctgcattgcg ccttcttcac gtaatctgtc agcaatggtc atcaagtttc 420
tccttttctt gtgggtgcgcg ttccgctatc tcaccaataa atgcacgaaa acgctgggca 480
tcccctgttt gtaatacgtg attaaacagg gcttttagct gtctgtcatt agtgktccct 540
gtaactagca g 551

<210> 454
<211> 93
<212> DNA
<213> Escherichia coli

<400> 454

tggcattctcg gtgtttgccga ttttcatgat atccagcccg ccggaaactt cttcccaaac	60
ggtttttgctg ttatccattg agtcacggaa ctg	93

<210> 455
 <211> 232
 <212> DNA
 <213> Escherichia coli

<400> 455	
cgtgccgaga tgatcctgta accatcatca gttgtgaagt agtgattcac gacttcaagg	60
cgcttttcaa aagggtatgt tggctttgac atattagggg ctattccatt tcacgtcca	120
acaaaatggg tgcagtacat actcgttggg aatcaacaca ggaggctggg aatgccgcag	180
aaatatagat tactttcttt aatagtgatt tgtttcacgc ttttattttt ca	232

<210> 456
 <211> 713
 <212> DNA
 <213> Escherichia coli

<220>
 <221> misc_feature
 <222> (1)...(713)
 <223> n = A,T,C or G

<400> 456	
ttagnngatn naangcccac ancctcgang gatctaggag gtagaatagc ttcgaattcc	60
ccagcagagc gcggccttct tcgtcagatt tcgcagtagt ggtaatggta atatccaaac	120
cacgaacgcg gtcgacttta tcgtagtcca tttctgggaa gatgatctgc tcacggacac	180
ccatgctgta gttaccacga ccgtcgaaag acttagcgga caggccacgg aagtcacgga	240
tacgaggtac agcaatagtg atcaggcgct caaagaactc ccacatgcgt tcgccacgca	300
gagttacttt acagccgatc ggatagccct gacggatttt gaagcctgca acagatttgc	360
gtgctttggg gatcagcggg ttttgaccgg agattgctgc caggctctgct gctgcgttat	420
ccagcagttt tttgtcagcg atcgcttcac caacacccat gttcaggggtg atcttctcga	480
cccaggggac ttgcatgaca gaattgtagt taaactcagt catgagtttt ttaactactt	540
cgtctttgta gtaatcatgc agtttcgcca tcgtactact ccatgtcggg gaacgctctc	600
ctgagtagga caaatccgcc ggagccggat ttaacgttgc gaacaaccgn cccggagggg	660
tggnggcagg accccgccat aactggcagc attaaattaa gcagaaggcc atc	713

<210> 457
 <211> 292
 <212> DNA
 <213> Escherichia coli

<400> 457	
tgaacagcag agatacggcc agtgcgccca atgttttttg tcctttaaac ataacagagt	60
cctttaagga tatagaatag gggatatagct acgccagaat atcgattttg attattgcta	120
gttttttagtt ttgcttaaaa atattgtagt ttttattaaa tgcaaaaacta aattattggg	180
atcatgaatt tgttgtagtga tgaataaaaat ataggggggt atagatagac gtcattttca	240
taggggtata aatgcgacta ccatgaagtt ttttaattgaa agtattgggt tg	292

<210> 458
 <211> 282
 <212> DNA
 <213> Escherichia coli

<400> 458	
ttattaaatg caaaactaaa ttattgggtat catgaatttg ttgtatgatg aataaaatat	60

agggggggtat	agatagacgt	catttttcata	gggtttataaa	tgcgactacc	atgaagtttt	120
taattgaaag	tattgggttg	ctgataattt	gagctgttct	attcttttta	aatatctata	180
taggtctgtt	aatggatttt	atttttacaa	ttttttgtgt	ttaggcatat	aaaaatcaac	240
ccgccatag	aacggcgggt	taaaatattt	acaacttagc	aa		282

<210> 459

<211> 300

<212> DNA

<213> Escherichia coli

<400> 459

tctgcgttcc	gctaaaaggt	gcaaatgctc	aggacgttgc	agcgttttgc	gtgaccgctc	60
ggggaaggca	aaattgcctc	tgggaaagca	ttgcgcgggg	tccggcgctc	atcaacaatc	120
ggggggcagc	aaggggctga	aacgggaaag	cccctcccga	agaaggggcc	ttgtataagg	180
aaagggttat	gatgaagctc	gtcatcatac	tggttgtgtt	gttactgtta	agtttcccga	240
cttactaaca	actcatcaga	ggggggagaa	atcctccctt	acccttggtc	ctttactcta	300

<210> 460

<211> 293

<212> DNA

<213> Escherichia coli

<400> 460

cggggtccgg	cgctcatcaa	caatcggggg	gcagcaaggg	gctgaaacgg	gaaagcccct	60
cccgaagaag	gggccttgta	taaggaaagg	gttatgatga	agctcgtcac	catactggtt	120
gtgttggtac	tggttaagttt	cccgaactac	taacaactca	tcagaggggg	gagaaatcct	180
cccttaccct	tggttccttta	ctctagggtg	aaaaaacaac	agcgtcaata	ggcctgccat	240
gtacgaagcg	agatctgtga	accgctttcc	ggttagcctt	ttttatcctg	ttg	293

<210> 461

<211> 359

<212> DNA

<213> Escherichia coli

<400> 461

caacacagga	ggctgggaat	gccgcagaaa	tatagattac	tttctttaat	agtgatttgt	60
ttcacgcttt	tattttttcac	ctggatgata	agagattcac	tgtgtgaatt	gcatattaaa	120
caggagagtt	atgagctggc	ggcgttttta	gcctgcaa	tgaaagagta	agagtcttcg	180
gcgggaaatt	attcccgcct	tacttacggc	gttgcgcat	ctcattgcac	ccaaatttat	240
tcttcacaaa	aataataata	gattttatta	cgcgatcgat	tattttattc	ctgaaaacaa	300
ataaaaaaat	ccccgccaaa	tggcagggat	cttagattct	gtgcttttaa	gcagagatt	359

<210> 462

<211> 673

<212> DNA

<213> Escherichia coli

<400> 462

gcaacccatg	tcctgacctg	ggttcggggg	acaccaaaaac	gtgccgagat	gatcctgtaa	60
ccatcatcag	ttgtgaagta	gtgattcacg	acttcaaggc	gcttttcaaa	agggtatttt	120
ggctttgaca	tattaggggc	tattccattt	catcgcccaa	caaaatgggt	gcagtacata	180
ctcgttgga	atcaacacag	gaggctggga	atgccgcaga	aatatagatt	actttcttta	240
atagtgat	gtttcacgct	tttatttttc	acctggatga	taagagattc	actgtgtgaa	300
ttgcatatta	aacaggagag	ttatgagctg	gcggcggttt	tagcctgcaa	attgaaagag	360
taagagtctt	cggcggggaa	ttattcccgc	cttacttacg	gcgttgcgca	ttctcattgc	420
acccaaattt	attcttcaca	aaaataataa	tagattttat	tacgcgatcg	attattttatt	480
tcctgaaaac	aaataaaaaa	atccccgcca	aatggcaggg	atcttagatt	ctgtgctttt	540

aagcagagaa	tacaggctgg	ttacgttacc	agctgccggg	ccttttagcgc	cgcttttcgat	600
ggtgaaggac	acttttctgac	cttcgtccag	agattttgtaa	ccatcgttct	ggatagcaga	660
gaagtgtacg	aac					673

<210> 463
 <211> 630
 <212> DNA
 <213> Escherichia coli

<400> 463						
tggtggcatt	ggttgctgga	gagagaaaac	ccccgcacgt	tgcaggtatg	cacctgacaa	60
caccacgggg	gctaattctt	actctagacc	actcaagaat	agccgcgaaa	cgttgtcatt	120
acaacacagg	cggctatatg	acgttcgcag	agctgggcat	ggccttcttg	catgatttag	180
cggctccggt	cattgctggc	attcttgcca	gtatgatcgt	gaactggctg	aacaagcgga	240
agtaacgtgt	catgcgggcg	tcaggctgcc	gtaatggcaa	tttgcgcccg	gaccaggccg	300
caggggggaa	actctgcggc	ctttttcgtt	cttactgcgg	gtaaggcacc	cagtcgcccgc	360
cgttcaggcg	aacgtacggt	ttatcctggt	attgaataac	tactgcattt	gagttctcgg	420
agaccgggtgc	tgtttgtggc	aacccactgg	tgagtttttt	ccagtcaaca	ttgtcttcgg	480
tgaaaatcctt	gccatcgaga	acgcgaacca	ccagatcgga	gatagccagg	aagctgctcg	540
gttgttcgat	gacaatcggt	gccccctgat	gcggtgcctt	catgccgaag	aatttcaccc	600
caacggggac	gtcgggtgata	gacgggctag				630

<210> 464
 <211> 391
 <212> DNA
 <213> Escherichia coli

<400> 464						
ctcaggctgc	tgattgtttt	tttgtgcaat	ggcgcggtat	tagcgtcgtt	gctgtcgatg	60
gagagaatca	taaactgtgt	gaatgatgat	tgttagcaag	gaaaactgtc	aaaaatcttc	120
aaaaaatttg	agggataagg	ccggaatggc	tccggccaga	gggaagttaa	ccgcgaagct	180
gttgctgctt	gagggtcgtt	ttaaccagac	gccaggcgct	ccatacgcca	aaaccgcgtc	240
tggcccagcg	gaccagcata	ttaggatggc	gaatcgtcca	gatcgccatc	acgctactgc	300
caaccagcgc	ccaggagcgc	agacttagca	gcatattcca	gcgacgatcg	taagcgcttg	360
ttgtctccag	ccattcacga	cgactggcgg	a			391

<210> 465
 <211> 625
 <212> DNA
 <213> Escherichia coli

<400> 465						
aacacaccac	accataaacg	gaggcaaata	atgctgggta	atatgaatgt	tttaatggcc	60
gtactgggaa	taatttttatt	ttctgggtttt	ctggccgcgt	atttcagcca	caaatgggat	120
gactaatgaa	cggagataat	ccctcaccta	accggcccct	tgttacagtt	gtgtacaagg	180
ggcctgat	ttatgacggc	gaaaaaaaaac	cgccagtaaa	ccggcggtga	atgcttgc	240
ggatagattt	gtgttttggc	tttacgctaa	caggcatttt	cctgcactga	taacgaatcg	300
ttgacacagt	agcatcagtt	ttctcaatga	atgttaaacc	gagcttaaacc	tcgggttaac	360
acattttgtt	cgtcaataaa	catgcagcga	tttcttccgg	tttgcttacc	ctcatacatt	420
gcccgggtccg	ctcttccaat	gaccacatcc	agaggctctt	caggaaatgc	gcgactcaca	480
cctgctgtca	cggtaatgtt	gatatgccct	tcagaatgtg	tgatggcatg	gttatcgact	540
aactggcaaa	ttctgacacc	tgacagacat	gcttcttcat	cattagccgc	tttgacaata	600
atgataaatt	cttcgcccc	gtagc				625

<210> 466
 <211> 623
 <212> DNA

<213> Escherichia coli

<400> 466

tgcttttgaa	tatgtgctcg	caatcttgag	aaggaaatgg	cgaccacgaa	agaaaaggca	60
aaaacgataa	tctgaaagag	ccaaggtatt	tcagtataag	cattgaatgc	gacagtaaac	120
tctttcggta	tcagccagag	agtgagacca	aaaatgataa	tcgtatacat	aagtctttcg	180
agtggctcgt	tagcaaaaag	tttcaacaat	ggagtaaata	catccaacat	atcaataact	240
ctcaactgta	agggatttga	aatgttaaca	caagctctcg	ctgtaggggt	atagccgaga	300
ccaccgaagc	ccggagggtg	tgaataaaaa	ccgggcacaa	cacgaaggcg	catttccgat	360
atccataaag	agtcggctct	gtctgttaaa	tttaaatgg	gggagtgcgc	ctccggttgt	420
aaataacgac	attgctgtgt	gtagtcctgg	cggcatcagt	ttttttcttg	aagttcggct	480
gatgtccgcc	ctttttaaag	tgaattttgt	gatgcggtga	atgcggctaa	gcgcacgtgg	540
cacagttaaa	agtcattgta	gtccttattg	gtttgggtgg	gaaagccgac	tgtattgtt	600
aactggttgc	agtcacctgg	agg				623

<210> 467

<211> 234

<212> DNA

<213> Escherichia coli

<400> 467

tgtttactta	caagagattc	atctttgtat	aaataaagat	aagtaattac	gcataaaaca	60
acaatgatta	taatagcaaa	aataaatatt	atcatctttg	atagattact	tgagatagcc	120
agcatcttgt	aaagccttta	tcgttttttt	atgctctgga	ttaatataat	cactacatct	180
atctgagcaa	tctgttggtg	atggacatgt	caacccatgg	tcatttacag	ccaa	234

<210> 468

<211> 529

<212> DNA

<213> Escherichia coli

<400> 468

attagctatt	tcggctaaaa	tagagactac	atgtcttcgg	tccatctcac	ttaaggagtg	60
tagttccggt	gtaagttttt	ccatagcttg	cactgctaaa	tttcgaacaa	ggaattttct	120
gctggtaatc	tctaaaaaga	tggcatggtt	tacaatgatt	tttgtttcct	tttgattatt	180
atgaacaact	gtccatgatt	tcgtttaaga	atgaagagaa	atcactaaac	gaactgaata	240
tattttctgt	gccaatatta	tctctaattt	caaaaaagtt	acttttaatg	tcggtaatga	300
ctccaactta	ttgatagtgt	tttatgttca	gataatgcc	gatgactttg	tcatgcagct	360
ccaccgattt	tgagaacgac	agcgacttcc	gtcccagccg	tgccagggtg	tgccctcagat	420
tcaggttatg	ccgctcaatt	cgctgcgtat	atcgcttttc	cttatcagtt	cgttgatgtc	480
agtggttttg	accacgaggg	agcttcacgc	gagttattga	aaaccctga		529

<210> 469

<211> 261

<212> DNA

<213> Escherichia coli

<400> 469

caaagaacct	tcaacatgaa	aaatatccat	ttgtttgcaa	aaaaagatta	ttaggaagga	60
aattaatgca	attatcgaaa	attcaaaaaa	tatccaaaaa	tagtatactt	tattccagaa	120
gagttcaata	taatgtttgt	cttcaatttt	tcttacttca	gggtaatata	gattgctcat	180
tacattgtga	gcttcatctt	tatttaattt	tctgttgact	ccagctctcc	gtgataacgg	240
ttttataatt	agatgcttat	c				261

<210> 470

<211> 98

<212> DNA

<213> Escherichia coli

<400> 470

agatgattgc	cgggaacttg	ttagcggcac	gcaggcggcg	gctcgcaccc	ttaccctgct	60
ctttacgtac	ttctgcgttg	atagtaaaca	tttctttc			98

<210> 471

<211> 259

<212> DNA

<213> Escherichia coli

<400> 471

agcgcgaacg	aagtcgatgt	gctgcagctt	cggttttgtac	gggtgacgct	gtacgtcctg	60
agctttaact	ttgattttctt	taccgtcaac	aacgatggtc	agaacttcgc	tgtagaattc	120
agcttttagct	tgcatgttca	tgactttgtc	gtgatccagc	tcgatagcca	gcggcgcttc	180
tttgccaccg	tagatgattg	ccgggaactt	gttagcggca	cgcaggcggc	ggctcgcacc	240
cttaccctgc	tctttacgt					259

<210> 472

<211> 94

<212> DNA

<213> Escherichia coli

<400> 472

aaaaacggcg	taaagaaagg	atgcaaacat	gttaataaaa	actcaaattg	atcccacgta	60
tatattacgc	cgcaaaatcc	ttacaataaa	cagg			94

<210> 473

<211> 174

<212> DNA

<213> Escherichia coli

<400> 473

ttaattatta	aaatagtgtg	acgcgattat	gtgggttatgg	gggtaaacat	taaataaacc	60
agcggggagg	ggaggtaaag	tgaaaaaata	aaaagcggat	aatcttaata	agcaggccgg	120
acagcatcgc	catccggcac	tgatacgagg	tttatttcag	ctcatcaacc	atcg	174

<210> 474

<211> 138

<212> DNA

<213> Escherichia coli

<400> 474

ctgtaaaaac	gtcaaaaaga	gtgtttttatc	aacagaagaa	tggaggctctg	acagatagta	60
gtaatgcaaa	aaaatggaga	cttaagttga	atgaacggga	gtaaagcgaa	aagactatag	120
agtgaaggag	aaattccc					138

<210> 475

<211> 191

<212> DNA

<213> Escherichia coli

<400> 475

tttgttggct	taatattcta	ttgttatctt	tatttataga	tgtttatatt	gcatgagggtg	60
gtttttggag	agaagaatga	ggaagatgcg	tcgagccaca	gaaacgtag	ctttacatat	120
agcggagggtg	atgtgaaatt	aatttacaat	agaaataatt	tacatatcaa	acagtttagat	180
gctttttgtc	g					191

<210> 476
 <211> 245
 <212> DNA
 <213> Escherichia coli

<400> 476
 cggccatttta tacaggaaaa gcctatgtca gaacgtaaaa actcaaaatc acgccgtaat 60
 tatctcggtta aatgttcctg cccaaactgc acccaagagt cagaacacag tttttcaaga 120
 gtacaaaaag gtgccctttt gatctgccct cattgcaaca aagtattcca gacaaatctt 180
 aaagctgtag cctgattgat tttattagta acaagtattt tttatatattt aataatatat 240
 ttaaa 245

<210> 477
 <211> 319
 <212> DNA
 <213> Escherichia coli

<400> 477
 aaattttcag gtaccttgtc accatacttt tttttctgag cattaatgat attttgagct 60
 tcttgaggat ctttaactcc ccacatttgg tggaaagtat tcatattaaa aggaagggtg 120
 aataatttgt ctttataaat cgccagtggg gaattagtaa aacgattaaa ttctactaaa 180
 tcattaacgt aatcccatat atatttatca ttggtatgaa aaatatgtgc accatattta 240
 tgaatctgga taccctcaca gtectctgtg tacgcatttc caccgatatg atttcttttc 300
 tcaatcacta aaacttttt 319

<210> 478
 <211> 149
 <212> DNA
 <213> Escherichia coli

<400> 478
 gcagtgatcg aagcgatgac gaagtgtatg gaaaaatcag aaaaactcag caaatcctga 60
 tgactttcgc cgacgctcag gccgccactt cgggtgcggtt acgtccggct ttctttgctt 120
 tgtaaagcgc caaatctgcc gatttcaac 149

<210> 479
 <211> 330
 <212> DNA
 <213> Escherichia coli

<400> 479
 gaaagtatct tcgttattga catcactgga aaatataact tgcttttcat tattaactc 60
 gaagcgcgta ccgtatctgg acaaacattt atcgagctta ccaaattcct gaagagggtt 120
 aactacagat aacatttgcg cgtcctttgc agtaatgccc gtcaaactcct tgacgggcat 180
 tatttagatt aaattaccag tatttcttcg gagtgaagaa tattaccagg tatatttaac 240
 acccacgttc gcggaccagt cttgatctac gtcaccacca ccgaggtagt tagcatcggt 300
 ataggcgctg aagttcttgg tgaagctaaa 330

<210> 480
 <211> 191
 <212> DNA
 <213> Escherichia coli

<400> 480
 tttttttcca gcaacggagc aaaagggttg cccttggtgca gctcagggtt aaccacttta 60
 actacgtggc gacgaccggg agatgtcggg ttacatttaa caactgccat tgtattactc 120

ctccgactta ctcagcgccg ccaacgaagt ccagattctg gccttctttc agggtgacgt	180
aagctttttt c	191

<210> 481
 <211> 188
 <212> DNA
 <213> Escherichia coli

<400> 481	
tccctttaac taccaggggtg ttaacgactt cgacttcgac ttcaaacagt ttctgcacag	60
cagctttgat ttctgctttg gtcgcttctt tagcaacttt gactacgatg gtgttgatt	120
ttccatcgc agtagacgct ttttcagaaa cgtgcggtgc acgcagcacc ttcagcagac	180
gttcttca	188

<210> 482
 <211> 172
 <212> DNA
 <213> Escherichia coli

<400> 482	
caaaggcgaa caaagcctgt gaagcccgaa ggctccacag acagtgcctac ttgaaggcct	60
tactgtttct tcttaggagc gaggaccatg atcatctggc ggccttcgat cttcgttggg	120
aaggattcga ccaactgccag ttcttgcaaa tcgtctttca cgcgattaag ca	172

<210> 483
 <211> 266
 <212> DNA
 <213> Escherichia coli

<400> 483	
tggagaaaac ggggtgattga taaagcaatc atcgttctag gggcgttaat tgcgctgctg	60
gaactgatcc gctttctgct tcagcttctg aactgatagc ggaaacgtaa ttaagggcta	120
agagcacact actcttagcc ctttaacatt taacgcattg tcacgaactc ttctgccgcc	180
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 <211> 259
 <212> DNA
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aacaccgata accattgagt tcagcagggc acgcgcggtg ccagcctgtg cccaaccgtc	180
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atcgttgaga gtacgagtc	259

<210> 485
 <211> 73
 <212> DNA
 <213> Escherichia coli

<400> 485	
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ccgtttaccg ggg	73